

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 10:47:52 ; Search time 3748.51 Seconds

(without alignments)
11147.724 Million cell updates/sec

Title: US-09-787-559-1

Perfect score: 2533
Sequence: 1 ggcaccgcagcgcgcgcga.....aaaaaaaaaaaaaaaaaaaaa 2533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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36: em_hlg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2533	100.0	2533	6 AX024729	AX024729 Sequence
2	2532.8	99.6	2632	6 AX024732	AX024732 Sequence
3	2326.6	91.9	2361	6 AX166527	AX166527 Sequence
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5	1585.8	62.6	4092	10 AF106937	AF106937 Rattus no
6	1522	60.1	4498	10 MM011494	MM011494 Mus muscu
7	1060.2	41.9	5115	5 AF219232	AF219232 Gallus ga
8	511.4	20.2	4868	6 AX086548	AX086548 Sequence
9	511.4	20.2	4868	6 HSM801732	AL136654 Homo sapi
10	511	20.2	5163	6 AX056393	AX056393 Sequence
11	509.8	20.1	2213	6 AK000396	AK000396 Homo sapi
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ALIGNMENTS

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LOCUS AX024729 Sequence 1 from Patent WO0017232.
DEFINITION AX024729
ACCESSION AX024729
VERSION AX024729.1 GI:10184808
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2533)
AUTHORS Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.
TITLE Regulatory protein from human keratinocytes
JOURNAL Patent: WO 0017232-A 1 30-MAR-2000;

REINARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)
; SCHAEFER BIRGIT (DE) ; WALLICH REINHARD (DE)
FEATURES
source location/Qualifiers
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DEFINITION Sequence 4 from Patent WO0017232.
ACCESSION AX024732
VERSION AX024732.1 GI:10184809
KEYWORDS
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Walllich,R.
TITLE Regulatory protein from human Keratinocytes
JOURNAL Patent: WO 0017232-A 4 30-MAR-2000;
REINARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)
; SCHAEFER BIRGIT (DE) ; WALLICH REINHARD (DE)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2524; Conservative 0; Mismatches 2; Indels 0; Caps 0;

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Qy 188 aaaaataatgtataaacaacagattagattcaagaactttggagaaatactatcgtaggt 247
Db 287 AAAAATAATGTGATAAACACAGATTAGATTCAAGCAATTTGGAGAAATCTATCTTAGAGT 346
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ACCESSION	AX166527			
VERSION	AX166527.1	GI:14546872		
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ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 2361)			
JOURNAL	Flanagan,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,			
FEATURES	Novel human protein kinases and protein kinase-like enzymes			
source	Patent: WO 0138503-A 18 31-MAY-2001;			
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Oy 1695 ttggaagagctgtctgtccctctgcagctctcaggaaggagcgcggtctgcgaacc 1754
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Db 1741 TCACTGACTCAAGGGCTGAAGGCTTTCGCGACAGCTGAGGAAGACACGCGGACCAA 1800
Oy 1815 ggttcttggagctgaacaaataaagggtgtgtgcaggtgtgtccaggttccctggc 1874
Db 1801 GGTCTTGTGGACTGAACAATAATCAAGGGCTGTGCTGCCAGTGTGCCAGGCCCTCCGCC 1860
Oy 1875 agccgggcaagcagggcgcgctgagcccttcacagccctctgacagagccagagcctg 1934
Db 1861 AGCCGGGCGACAGGGCGGCGCTTACGCCCTTCCACGCCCTCTGACAGAGCCAGGGCTG 1920
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RESULT 4
AB020480
LOCUS AB020480 2650 bp mRNA ROD 06-AUG-1999
DEFINITION Rattus norvegicus mRNA for salt-inducible protein kinase, complete cds.
ACCESSION AB020480
VERSION AB020480.1 GI:5672675
KEYWORDS SIK; salt-inducible protein kinase.
SOURCE Rattus norvegicus (strain: Sprague-Dawley) 6 week old male adrenal gland cDNA to mRNA.


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Db 1379 CTCCCCAGAGCCTGCTGGACACAGCTATCAGTAGAGAGGCCGAGGCTCCACCT 1438
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Db 2189 CCAGCCCGCATCTCCCGCTGCGCTGTCCCGGCACTCTCGATGCCACCTGTGCACAT 2248
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RESULT 5
AF106937
LOCUS
DEFINITION
Rattus norvegicus protein kinase KID2 (Kid2) mRNA, complete cds.
ACCESSION
AF106937
VERSION
AF106937.1
KEYWORDS
Norway rat.
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 4092)
AUTHORS
Feldman,J.D., Vician,L., Crispino,M., Hoe,M., Baudry,M. and
Herschman,H.R.
TITLE
The Kid2 gene encodes a protein kinase induced by depolarization in
brain
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 4092)
AUTHORS
Feldman,J.D., Vician,L., Crispino,M., Hoe,M., Baudry,M. and
Herschman,H.R.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-1998) Pediatrics, UCLA, 10833 Le Conte Ave., Los
Angeles, CA 90095-1752, USA
FEATURES
source
1..4092
location/Qualifiers
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/db_xref="GI:6492128"
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GMSFHTTPAVSSGLQCTASSRGRSLLEVLHQQLDLDLQHSVAVSDDQAPQPLSP
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BASE COUNT
856 a 1161 c 1102 g 973 t

ORIGIN

Query Match 62.6%; Score 1585.8; DB 10; Length 4092;
Best Local Similarity 79.2%; Pred. No. 4.1e-288;
Matches 1994; Conservative 0; Mismatches 462; Indels 61; Gaps 7;
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QY	194	aattgatataaacagattagattcaagaacaattggagagaatctatcgtgaagttcagct	253
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QY	254	gatgaagctcttgaacatcacacacatcataaagctttacagattatlgaaacaaga	313
DB	360	CATGAACCTCTGAAACCAACCAATATTATCAAGCTTTACAGGTTATGAGACAAAGA	419
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QY	554	agagcctctgtccacgttgatgttgggaagccccccgtatgcgcgccccggaagctcttgag	613
DB	660	GAAGCCTTGCTACTTGTGTGGAGACCCCCCTATGCTGCTCCGAGTCTTTGAGGG	719
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DB	720	GAAAGAGTATGAAGGTCCCAAGCTGGACATCTGGACCTCGGCTGTGCTTATGTCTCT	779
QY	674	gltctcggtctcttccccccttgaatggcccttaacccctgcgaagcttbaagacagcgtgtct	733
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QY	734	ggaggggcgcttccgcatccccctctctcatgttctcaagaatgtagagcctgataccgcg	793
DB	840	GGAAGGCGGTTCCGCATCCCTCTTTCATGTCTCAAGACTGTGAGACACTATCATGACG	899
QY	794	catgctgtgttggaacccgcgaagcgcatcacatcgcgccagatccgcgcgaacagcagctg	853
DB	900	CATGCTGTATGTGAACCCCGCCCAAGCGCATACACATTGTGCCAGATCCGCACACCGATG	959
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DB	960	GATGAGGCGCCAGCCCAACCTCTCTGCGAGCAGACGACCTGCCTTCTCCATCAGAGGCTA	1019
QY	914	caacctcaaaccttggcgagcatagatagaagcagcgctcgggtatcatgacgaaccttggcgt	973
DB	1020	CACCTCCAACTGGGCGACATCAACAAGCAGAGGTGCTGGGCAATCAATGCAAGGCCCTGGGCAT	1079
QY	974	ggaaccgcaagagacgcttggaagtcactgtgcaaaacagcagctataacacacttgcctgcat	1033
DB	1080	CGACCGGCAAGAGGACATTAAGTCTCTACAGAAACAGCACTTCAACACCACTTTGCGGCTAT	1139
QY	1034	ttattaaactctctcttgaagcgcttcaagagatctcgnaatgctcag-----tgctc	1084
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QY	1085	cgcgcgcgcgcgttgcgaagcgaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1144
DB	1200	CACCCCTGCACCTTCCGACGAAGCTTCAAGCTCCGAAATCTGACACCTTCACACAGCTTGGAGT	1259
QY	1145	gactcgaagaaggtcttcttcaacgcgaaccttctcgaacctgtgtctgttccgcgaacgcga	1204
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QY	1325	gtccccaagcagctbctgtgacacagccatcaatgtagaagccagcgagggccgagccct	1385
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QY	1385	agaagaagaagacaacagcagagctccctgcgcgaagacagagggcgagacacctt	1444
Db	1497	GGAGAGGAGACGAGGAGGTCTCGAGAACCCCTGCTGGCAGACTGCGCCGAGAACATACAT	1555
QY	1445	ggcgaagcttccaacccgcctctcccactaacgcgcga tatalagctgtccctc	1504
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QY	1505	caccacggcaagttcctgtcgagaggaaacagctctgacagtgtgtctgaactctcttcgag	1566
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QY	1745	gtcggacaacctcactgactcaagaaggtctgaagcctlttcgacagcagctgaggaagaacac	1804
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	OY	2342	ctgtcccttaggcagcttgcctgylga	c	ggcagccctgcacatccttgcaaggac		2401
	DB	2427	TGGCCAGCGGGGAGAGTTCGTCGTG	A	CTGACGTGAGGAGTACTTGCACACCC	TC	2486
	OY	2402	actgactc-----ttacagaataa	a	acttcgaagagtlaaga---catctg		2445
	DB	2487	CCCACCCACGAGTGGACTCTTC	CA	GAAATAAATTTCAGCATGTGAAGATG	TT	2546
	OY	2446	gccccaagcgcaagaactctctaga	a	ggcataaataacatcagtaagtgcttgc		2502
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	LOCUS	MWU11494	4498 bp	mRNA	ROD	29-OCT-1999	
	DEFINITION	Mus musculus protein kinase		mRNA, complete cds.			
	VERSION	U11494					
	KEYWORDS	U11494.2	GI:6137751				
	SOURCE	house mouse.					
	ORGANISM	Mus musculus					
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	AUTHORS	Mammalia; Euthelia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
	TITLE	1 (bases 1 to 1434) Ruiz,J.C., Conlon,F.L. and Robertson,E.J. Identification of novel protein kinases expressed in the myocardium of the developing mouse heart Mech. Dev. 48 (3), 153-164 (1994)					
	JOURNAL	9520078					
	MEDLINE	2 (bases 1 to 1434)					
	REFERENCE	Ruiz,J.C.					
	AUTHORS	Direct Submission					
	TITLE	Submitted (27-JUN-1994) Joseph C. Ruiz, Molecular and Cellular					
	JOURNAL	Biology, Harvard University, 16 Divinity Ave, Cambridge, MA 02138,					
		USA					
		3 (bases 1 to 4498)					
	REFERENCE	Ruiz,J.C.					
	AUTHORS	Direct Submission					
	TITLE	Submitted (28-OCT-1999) Wells Center for Pediatric Research, Riley					
	JOURNAL	Hospital for Children, Indiana University School of Medicine, 702					
		Barnhill Drive, Room 2616, Indianapolis, IN 46202, USA					
		Sequence update by submitter					
		On Oct 28, 1999 this sequence version replaced gi:595420.					
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 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus

REFERENCE
 AUTHORS Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,Y.
 TITLE The new serine-threonine kinase, qik, is a target of the qin oncogene
 JOURNAL Biochem. Res. Commun. 276 (2), 564-570 (2000)
 MEDLINE 20484194
 PUBMED 11027514
 REFERENCE
 AUTHORS 2 (bases 1 to 5115)
 TITLE Direct Submission
 JOURNAL Submitted (27-DEC-1999) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

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Sugen, Inc. (US)
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 LOCUS
 DEFINITION Homo sapiens CDNA FLJ20389 fls, clone KIAA4591, highly similar to
 AB018324 Homo sapiens mRNA for KIAA0781 protein.
 ACCESSION AK000396
 VERSION AK000396.1 GI:7020457
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens ileal mucosa CDNA to mRNA, clone_1lb:kala
 clone:KIAA4591.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K.,
 Hirao, M., Ohmori, Y., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
 Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
 NEDO human cDNA sequencing project
 unpublished (2000)
 2 (bases 1 to 2213)
 TITLE
 JOURNAL Submitted (15-FEB-2000) to the DDBJ/EMBL/Genbank databases. Sumio
 Sugano, Institute of Medical Science, University of Tokyo, Department
 of Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)
 COMMENT
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan. cDNA full insert
 sequencing. Research Association for Biotechnology. cDNA library
 construction. 5' - 3' end pass sequencing. Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).

FEATURES
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VERSION AC012140.3 GI:7341873
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 148463)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

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TITLE
JOURNAL
REFERENCE
AUTHORS
Homo sapiens, clone RP11-10M14
Unpublished
2 (bases 1 to 148463)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Baran,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,D., Doyle,M.,
Ferreira,P., Fitzhugh,M., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,N.
Direct Submission
Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6454007.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
Project Information
Center project name: L3106
Center clone name: 10_M_14
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135488 bases at least Q40
Consensus quality: 141694 bases at least Q30
Consensus quality: 144517 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 146863; sum-of-ctnigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1122: contig of 1122 bp in length
* 1123 1222: gap of 100 bp
* 1223 2680: contig of 1458 bp in length
* 2681 2780: gap of 100 bp
* 2781 4940: contig of 2160 bp in length
* 4941 5040: gap of 100 bp
* 5041 6346: contig of 1306 bp in length
* 6347 6446: gap of 100 bp
* 6447 9361: contig of 2915 bp in length
* 9362 9461: gap of 100 bp
* 9462 13245: contig of 3784 bp in length
* 13246 16902: gap of 100 bp
* 16903 17002: contig of 3557 bp in length
* 17003 22603: gap of 100 bp
* 22604 22703: gap of 100 bp
* 22704 30328: contig of 7625 bp in length
* 30329 30428: gap of 100 bp
* 30429 35509: contig of 5081 bp in length
* 35510 35609: gap of 100 bp
* 35610 46431: contig of 10822 bp in length

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VERSION	AP001751.1				
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REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (sites)				
REFERENCE	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Pelleron,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schlichthabel,M., and Schudy,A. The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium Nature 405 (6784), 311-319 (2000)				
JOURNAL	20289799				
MEDLINE	2 (bases 1 to 340000)				
REFERENCE	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Pelleron,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schlichthabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamatsu,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstieck,G., Hornischer,K., Barand,P., Scharif,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S., Hennig,U., Risseimann,L., Dagand,E., Wehmaeyer,S., Borzjym, Gardner,K., Mizelc,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.L.				
TITLE	Direct Substansjon				
JOURNAL	Submitted (10-Apr-2000) to the DBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium * RIKEN Genomic				

COMMENT

Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBR, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)

On May 30, 2000 this sequence replaced g1:7717412

The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *

Sagamihara 228-8555, Japan,

- * e-mail: hallo@iegsc.riken.go.jp
- * URL: <http://hgp.gsc.riken.go.jp/>

and
* Institute of Molecular Biotechnology

Institute of Molecular Biotechnology, Senckenberg
Beutenbergstrasse 11, D-07745 Jena, Germany

* e.mail: gscj-submit@genome.lmb-jena.de
* URL: <http://genome.lmb-jena.de/>

and
* Keio University School of Medicine, Molecular Biology, * Tokyo

160-8582, Japan,
* e-mail: nshimizu@med.kyoto.ac.jp

* URL: <http://www.dmb.med.keio.ac.jp/>

and
* GBF, Dept. of Genome Analysis,

* Mascheroder Weg 1, D-38124
info.genome@bf.de

* URL: <http://genome.gbf.de/>

* Max-Planck Institute for Molecular Genetics

* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de

* URL: <http://chr21.rz-berlin.mpg.de/AL163296>: Submitted (10-Apr-2000)

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RESULT 15
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DEFINITION
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ACCESSION AC018734
VERSION AC018734.3 GI:8569950
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 179556)

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AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179556)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Jun 16, 2000 this sequence version replaced gi:7023168.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0351D02
----- Summary Statistics -----
Sequencing vector: M13; 1008
Sequencing vector: plasmid; 08
Chemistry: Dye-Primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170077 bases at least Q40
Consensus quality: 173263 bases at least Q30
Consensus quality: 175196 bases at least Q20
Insert size: 180000; agarose-fp
Quality coverage: 5.54 in Q20 bases; agarose-fp
Quality coverage: 5.64 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 2355: contig of 2355 bp in length
* 2356 2455: gap of unknown length
* 2456 6730: contig of 4275 bp in length
* 6731 6830: gap of unknown length
* 6831 17211: contig of 10381 bp in length
* 17212 17311: gap of unknown length
* 17312 30665: contig of 13354 bp in length
* 30666 30765: gap of unknown length
* 30766 45152: contig of 14387 bp in length
* 45153 45252: gap of unknown length
* 45253 62956: contig of 17704 bp in length
* 62957 63056: gap of unknown length
* 63057 79924: contig of 16868 bp in length
* 79925 80024: gap of unknown length
* 80025 107432: contig of 27408 bp in length
* 107433 107532: gap of unknown length
* 107533 138094: contig of 30562 bp in length
* 138095 179556: contig of 41362 bp in length.
* 179557 179556: contig of 41362 bp in length.
FEATURES
source
1. 179556
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/clone="RP11-351D2"
1. 2355
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clone_end:SP6
vector_side:left"
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/note="assembly_name:Contig7"
6831..17211
/note="assembly_name:Contig8"
17312..30665
misc_feature

misc_feature /note="assembly_name:Contig9"
30766..45152
/note="assembly_name:Contig10"
45253..62956
misc_feature /note="assembly_name:Contig11"
63057..79924
misc_feature /note="assembly_name:Contig12
clone_end:T7
vector_side:right"
misc_feature /note="assembly_name:Contig13"
80025..107432
misc_feature /note="assembly_name:Contig14"
138094..179556
misc_feature /note="assembly_name:Contig15"
179557..179556
BASE COUNT 37079 a 49750 c 51365 g 40456 t 906 others
ORIGIN
Query Match 19.5%; Score 492.8; DB 2; Length 179556;
Best Local Similarity 99.4%; Pred. No. 4.1e-83;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Oy 1995 cagagctgctccagttcaagcaccacccgcgcgtgacccgcgtgtcccaagccccc
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Db 83155 CACAGCGCTCTCAGACTTACAGACACCCGGCGCTGACCCGGCTCTCCAGGCCCC
Oy 2055 cagcggcccttgcgcgtttgtatgccccctgtatgccccctgtgggctgacccgctc
|||
Db 83215 CAGCGGCCCTTGCCTCCCTTTGTATGCCCTCTGTATGGCTTGGGCTGCCCGCTC
Oy 2115 ccagcaccctctcaagctcgggctccgcgtgctgcgcgcgccacctctcgaagccg
|||
Db 83275 CCACAGCACCTTCTCAGCTGCGGGG-TCCCGGTGCTGCGCGCCCGCCACTCTCGAGACCGC
Oy 2175 gcttccccctgctgctgagcgagctcctctgagacacacctctgaattggacccg
|||
Db 83334 GCGTCCCGGTGGCTTCAAGCGCGCAGCTCTCGACACACCTCTCAGATTGGACCGCGC
Oy 2235 ccacccgccccctcgcgtgctcccccacacgacctgacagctgcccccaagttgtag
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Db 83394 CCCACCGCCCTTCCCGCTGCTGCCCCACACCGCTGCGGCGACAGCTGCGCCCAAGTTGTAG
Oy 2295 cccttgggctgctgcaaggaggactgtgagatgagagacctgtagcctgtccctaggc
|||
Db 83454 CCCCTGGGGCTGCTGACAGGGAGCTGATGATGAGACCTGATGCCCTGCTCCCTAGGC
Oy 2355 acgttgccttggctgcaatgaggagcgcctgcatccctggcagcgacactgacttaca
|||
Db 83514 ACGTTTGTCTGTGTCAGTGAAGGAGCGCTGCATCTGTGGACAGGACACTGACTCTTACA
Oy 2415 gcaataactcagaagaggttaagacatctgacctcaagccaagcaactctttagaagcg
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Db 83574 GCATTAACCTTACAGAGAGAGTGAAGACATCTGGCCCTCAAAAGCCAGAACTTCTAGAACG
Oy 2475 aaataagcaatcgtttagtgttttgc 2502
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Db 83634 AAATTAAGCAATACGTTAGGTGTTTGGC 83661
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Search completed: March 22, 2002, 13:29:28
Job time: 9696 sec

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Db 310 gttcgaactacatctttaaaccaggaagggttgaagagtgtaagctcgccgctcttcca 369
Oy 515 gcaaatccctgtcgccgttgagtaactgtacagccaaatcaatccatccatccaggaactcaa 574
Db 370 gagagttctgtctgcgttgactactgttcaacagcaaatggttgcacaaaggaactcaa 429
Oy 575 gaccgagaacccctctgttgatgtgcaacatgagacatcaagctgagattttgag 634
Db 430 gcaagagaacgtgtgtctgagacgcccagatgaatgtaagatagctgacttcgactc 489
Oy 635 gaattctacaagtgagagagcctctccctggtggtgtggaagcccccgatagcgcg 694
Db 400 taattatgtatcagaatgttgaaattcttaacgaactagctgtgtatgcacaaatlaagcagc 549
Oy 605 cccggaagctcttgagggaagaaatgaatgaagcccccagctgagacatctgagcctgg 754
Db 550 accggaagctcatcaggaagagctgtatgctgagctgtcgtgagttatcttgagctgtgg 609
Oy 755 cgtggtgtctgactgctgctgctgctgctctctcccttgaatgggctaactgagcagc 814
Db 610 tgtatctgtatgctcctctctctgtgcaacctcccggttcgacgaatgagcaagtgcttac 669
Oy 815 gctgagacagcggtgtctggaaggcgttccgcatccctctctcatgcttccaagactg 874
Db 670 gctcttaagaagaatcaggaagggtgtgttctcaacatcccgagatctccaacgcttctat 729
Oy 875 tgaagagctgtatccgagcatgtgtgtgtgagcccgacagcgacatccacatcgcca 934
Db 720 tgcactctgtgtatgacatgtgtcaggttgaccccttgaagcgagacatataaaga 789
Oy 935 gatccgagcagccggtgagat 955
Db 790 catcagagacatgaatggtt 810

```

RESULT 5
 US-09-101-146-44
 ; Sequence 44, Application US/09101146
 ; Patent No. 6124125
 ; GENERAL INFORMATION:
 ; APPLICANT: Dartmouth College, St. Vincents Institute of
 ; APPLICANT: Medical Research, Kemp et al.
 ; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jane Massey Licata, Esq.
 ; STREET: 66 E. Main Street
 ; CITY: Marlton
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: WINDOWS 95
 ; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/101.146
 ; FILING DATE: October 7, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PN7450
 ; FILING DATE: 8 JAN 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: 00-0050
 ; TELEPHONE: (856) 810-1515
 ; TELEFAX: (856) 810-1454
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1647

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; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-09-101-146-44

Query Match          7.3%; Score 191; DB 3; Length 1647;
Best Local Similarity 54.1%; Pred. No. 2e-31;
Matches 433; Conservative 0; Mismatches 365; Indels 3; Gaps 2;

Oy 158 gggccagagtcagggccagcaagaatccctccgggtgggttttacgacatcgaagcgagc 217
Db 3 GGCCGAGAAGCAGAGACAGACAGCGGGGTGAAGATCGGCCACTGACATCTGGGGACAC 62
Oy 218 cctgggcaaaaggaacttcggtggtgtgaagctggcgcgaatcgagtcaccaaaagca 277
Db 63 GCTGGCGCTCGGCACCTTCGGGAAAGTGAGGTGGGCAACGACGAGTTGACTGGACATTA 122
Oy 278 ggttcaataaaataatgtga-taaacagattagattcaagcaat--tggagaaat 334
Db 123 AGTTGCTGGAAGATTACTCAACCGGACAGAAATTTGAAGCCTGGACGTGTCGGGAAAT 182
Oy 335 ctatcgtgaggttcaagctgatatgaagcttctgaaccatccacacatcatataaagcttaca 394
Db 183 CCGCAGAGAGATCCAGAACCTGAACCTTTTCAGGCAACCTCATATATCAAACTGTACCA 242
Oy 395 ggtatggaacaaagagacatgcttataatgtaactgtgaatttgcataaaatgagaat 454
Db 243 GGTCAATCAGTACACCGTGTGATATTTTCATGCTCATYGAATATGCTCAGAGAGGAGACT 302
Oy 455 gttgatatttgaacttccaaagggcaacctgagtgagagcaggcggaagaagttctg 514
Db 303 ATTGATATTATATCTGTAATAAATGGAAGTTGACCAAAAGAGATGACGCTGTTTCCA 362
Oy 515 gcaaatccctgcgcgttgagagtaactgtcacagacatcatatgltccacccgagactcaa 574
Db 363 GCAGATCCTTCTGTGGTGGAGACTATTGTCACAGGCAATGTGTGTCCACAGAGATTGAA 422
Oy 575 gaccgagaacctctgctgagatgagcaacatgacatcaagctgagagatttgattgg 634
Db 423 ACCTGAAGAACCTCTGCTGTGATGACACACATGAATGCAAAAGATACCCGCTTCTGTTTC 482
Oy 635 gaattctacaagtcgaagagcctctgtccagtggtgtggaagcccccgatagcgcg 694
Db 483 AAACATGATGTCAGATGCTGAATTTTAAGAACGACGCTGTGCTGCCAATTAATGCTGC 542
Oy 695 cccggaagctcttgagggaagagatgaagagcccccagcttgagacatctggaagcctgg 754
Db 543 ACCAGAAGTAATTTACAGGAAGATTTCTACGCGAGGCCCTGAAGTACATCTGACAGCGG 602
Oy 755 cgtgtgtctgtaagctcctggtgtcgtgcttccctccttgatgagtgccaaactgcgcag 814
Db 603 GGTCAATCTCTATGCTTGTGCTGTGTAACCTCTCCCTTTGATATGACCAACGTCGCAAC 662
Oy 815 gctgagacagcggtgtctggaaggcgcgttccgcatccctctctcatgttctcaagctg 874
Db 663 TCTTTTAAGAGATATGTAGCGGATATTTTAACCCCTCAGTATTTGAATCCCTGTGT 722
Oy 875 tgaagacctgaatccgcgcatgtgtgtgtgtgagcccgcaagcgacatccacatcgcca 934
Db 723 AATTAAGCCTTTTGAAGCATATGCTGACGAGTAAGATCTATGAAGAGGCCACAAATTAAGA 782
Oy 935 gatccgagcagccggtgagat 955
Db 783 TATCAGGGAACATGAATGTT 803

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RESULT 6
 US-08-557-006C-44
 ; Sequence 44, Application US/08557006C
 ; Patent No. 6258547
 ; GENERAL INFORMATION:

* APPLICANT: Berl, Rajindar K.
 * APPLICANT: Carling, David
 * APPLICANT: Forder, Robert A.
 * TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
 * FILE REFERENCE: NGAP/PMH3/588/UST
 * CURRENT APPLICATION NUMBER: US/08/557,006C
 * CURRENT FILING DATE: 1996-03-06
 * PRIOR APPLICATION NUMBER: PCT/GB94/01093
 * PRIOR FILING DATE: 1994-05-20
 * PRIOR APPLICATION NUMBER: GB 9310489.1
 * PRIOR FILING DATE: 1993-05-21
 * PRIOR APPLICATION NUMBER: GB 9318010.7
 * PRIOR FILING DATE: 1993-08-31
 * NUMBER OF SEQ ID NOS: 44
 * SOFTWARE: PatentIn Ver. 2.1
 * SEQ ID NO 44
 * LENGTH: 1747
 * TYPE: DNA
 * ORGANISM: Human
 * FEATURE:
 * NAME/KEY: gene
 * LOCATION: (1)..(1747)
 * OTHER INFORMATION: Full length cDNA sequence fragment of human AMPK -
 * OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
 * OTHER INFORMATION: nucleotide 1765
 * OS-08-557-006C-44

Query Match	6.7%	Score 176	DB 4	Length 1747
Best Local Similarity	53.7%	Pred. No. 3e-28		
Matches 433	Conservative 0	Mismatches 365	Indels 8	Gaps 3

[illegible]

Db 603 gggtttatcccgatgtgccctctctctgtgagcaacctcccgcttgtagcagatgtgacacgtg 662

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Db 663 cctacgcctctttaagaaagatccgaggggtgtgtcttcacatacccgagatctccaacggt 722

QY 870 gactgtgagagccgtgataccgcacgatctgtgtgtgtagaacccgcacagcgcatcaaccatc 929

Db 723 tctatgtccaactcgtcgtgatgcacatgtctgcaggttggaaccccttgaaagcgagcaactatc 782

QY 930 gcccaagatccgcgcagcacccgtgtgac 955

Db 783 aaagacatacagagacatgaatgttct 808

RESULT 7
US-08-557-006C-37

Patent No. 5258547
GENERAL INFORMATION:
APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAR/PHM37588/USP
CURRENT APPLICATION NUMBER: US/08/557, 006C
CURRENT FILING DATE: 1996-03-06
PRIORITY APPLICATION NUMBER: PCT/GB94/01093
PRIORITY FILING DATE: 1994-05-20
PRIORITY APPLICATION NUMBER: GB 9310489.1
PRIORITY FILING DATE: 1993-05-21
PRIORITY APPLICATION NUMBER: GB 9318010.7
PRIORITY FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 1736
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat liver AMP
OTHER INFORMATION: protein kinase
US-08-557-006C-37

Query Match	6.78; Score 175.4; DB 4; Length 1736;
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[illegible]

Query Match	Best Local Similarity	Score	DB	Length
Matches 417; Conservative	6.7%;	175.4;	4;	1783;
		Pred. No 4e-28;		
		Mismatches 0;	Indels 381;	Gaps 1;
Oy	158	gggcagagatcagggccagagagagcctccggatgggttttacacatcagcgcgc		217
Db	4	ggcttgaagaagcagacagacagcggcgggttgaaatcgcacactacgttgcgtgcac		63
Oy	218	cctggcgaaagaaacttcgcggttggtaagctgcgcgcacgcgttcacccaagcga		277
Db	64	gctggcggttcgcacacttcgcgaagatgaaatttggaacacaaatlaacggccataa		123

Oy	278	ggttgcaataaaataatgata---	aaacagattgattcaagcaatttgganaaat	33
Db	124	agtgccagcttaataacttaatacagaagaattccgaattcagatgtgttgganaaat	180	
Oy	335	ctacgttgaggttcagctgataagctcttgaacacatccacatatataaacttacc	396	
Db	184	aaaacggaagaaattcaaaatcttaaaactcttcgtcaacctcatatatacaactacc	243	
Oy	395	ggtatggaaaacaaagagcatcgcttccatccgtccactgaatttgcgtataaatgtgaaat	454	
Db	244	ggtgcatcagcatcccaacagaattttttatgtaagtgaataatgcttgagtgaaat	303	
Oy	455	ggttgattatttgacttccaaaggcccccagtgagaagaaagagcgccgaaagatctcg	514	
Db	304	atttgactacatctgttaagacatgacggttgaaagatgaaagccagcgctcttca	363	
Oy	515	gcaaatctgtccgcccgttgagatgatacgaacacatcacatctgccacggagactca	574	
Db	364	gcagatctgtcgtctgtgattacccgtatagatattgttgttcatcgtgacctga	423	
Oy	575	gaccgaacacctctcgtatggaataatgacataaagcttcgagatttggattctgg	634	
Db	424	accagaaagatccgtctgtgagtcacaatgatgacgaagataagccgatttgcattc	483	
Oy	635	gaattctacaagtcagagagaccctcttccagtggtgttggaagccccgttaagccg	694	
Db	484	taataatgatgcatgacatgtagaattcttcgagaacaaagtctggatctccaattatgcgc	543	
Oy	695	cccgaagctcttgaggggaagagatataagccccccagcggacatctggagccggg	754	
Db	544	acctgaagcatctcagacgaattgtatcaggtcttcgaagtgtgattctggagctgtg	603	
Oy	755	cgtggtcgtgaagctccgtctcgtcgtggttccctcccttcagatgggctaactgcgaa	814	
Db	604	tgttatcttgtaagcctctcttctgttgcaacctcccatlttgatgataagacgttaacct	663	
Oy	815	ggttgagaacagcggtctcgtgaaagccgcttcgcgcgtccctcttcagtctcaaaagctg	874	
Db	664	gttatttaagaagatccgaggggtgtctttatatactccagaatatctcaatggttctgt	723	
Oy	875	tgaagacctatccgcgcgactctgtgtgttgaccccgcaagcgataccatcgccca	934	
Db	724	cgcacactctcctatgcatatgctgcagaggttgaccactgaacgagcaactataaaga	783	
Oy	935	gatccgcgaacacgggtgat	955	
Db	784	catagaagcatgaaatggtt	804	

```

RESULT 9
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MMLR1D701
; CLONE: 472480
; US-09-016-000-10

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Query Match 3.7%; Score 96.6; DB 2; Length 1929;

Best Local Similarity 51.3%; Pred. No. 1.5e-11;

Matches 250; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

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QY 159 gccacagatcagggccagcagaagtcctccggtgtgttttaccagacatcgagcgacc 218
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 320 gccacagcctccgcccgcgcctcggaagacgagcctgagcattcaggaaatc 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 219 ctgggcaaaagcgaacttcggtgtgtgaagctggcgcgcatcgatccaccaaacgag 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 380 cttggggaaagcgtcttcttccacggtgtcctgacgaactgcgaacctccacagaa 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 279 gtgcgaataaataatgtataaacac---gattagatccaagcatttggagaataatc 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 440 tatgccattttaaattctggagaaacgcatatctttaaagaaacagctccctatgta 499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 336 tatcgtgaggttcagctgataagcttcgtgaaccatcacacatcaataaagctttaccag 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 500 accagagacgggatgcatgctgcgcctggatcaccctcttcttggtaagctttacttgc 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 396 gtatggaacaaagagcagatcttaccatcgctcaactgaatttctaaataatgagaatg 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 560 acatttcagacacgacgaaagctgatttgcgcttattgacaaataatggaactga 619
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 456 ttgatatttgcacttcccaacgggcacctgagtgagaagagagcggaagaagttctg 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 620 ctttaattatatttgcgaataatcggttcatctgcatgagacgtgacccgatttttacacggct 679
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 516 caaatcctgtcggcgtgtgagtaactgtcacgacatcacatcgtccacggagactcaag 575
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DB 680 gagattgtctgctgttgaagattcttcacagggacgcatcttccacagggacctttaa 739
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QY 576 accgagaacctctctgtgtgtgcaacaatggaacatcaagcttgcagatttggattggg 635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 740 ccggaataacatttggtaaatgaaagattgcacatccagatccagatttttggaaacaga 799
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 636 aattctt 642
    |||||
DB 800 aaagtct 806

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RESULT 14

US-09-289-466-2

; Sequence 2, Application US/09289466A

; Patent No. 6124272

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION

; FILE REFERENCE: RTS-0060

; CURRENT APPLICATION NUMBER: US/09/289,466A

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; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 2
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1750)
; US-09-289-466-2

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Query Match 3.6%; Score 95; DB 3; Length 1890;

Best Local Similarity 51.1%; Pred. No. 3.3e-11;

Matches 249; Conservative 0; Mismatches 235; Indels 3; Gaps 1;

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QY 159 gccacagatcagggccagcagaagtcctccggtgtgttttaccagacatcgagcgacc 218
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 281 gccacagcctccgcccgcgcctcggaagacgagcctgaggaacttcaagtttggaaatc 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 219 ctgggcaaaagcgaacttcggtgtgtgaagctggcgcgcatcgatccaccaaacgag 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 341 ctggggaagcgctctttccacggtgtcctgtgcgcgagacatgcaacctccagagaa 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 279 gtgcgaataaataatgtataaacac---gattagatccaagcatttggagaataatc 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 401 tatgcattaaatcttcgtggaagcgacatacataaagagaacaggtccctatgta 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 336 tatcgtgaggttcagctgataagcttcgaaccatcacacatcaataaagctttaccag 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 461 accagagaagcggaatgcatgctgcgccttgatcaaccttcttgttaagctttacttc 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 396 gtatggaacaaagacatgctttacatcgctcactgaatttctaaataatgagaatg 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 521 acattcagagcagcgaataacatgatttgcgccttagttagtgcataaatgagaaacta 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 581 cttaaatatattcgaataatcggttcatctgataagacctgttaccgatttaccagct 640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 516 caaatcctgtcggcgtgtgagtaactgtcacgacatcacatcgtccacggagactcaag 575
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DB 641 gagattgtctgctttagaagtaactgtcacggaagggacatcattcaagggaccttaa 700
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 576 accgagaacctctctgtgtgtgcaacaatggaacatcaagcttgcagatttggattggg 635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 701 ccggaataacatttggtaaatgaaagattgcacatccagatccagatcttggaaacaga 760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 636 aattctt 642
    |||||
DB 761 aaagtct 767

```

RESULT 15

US-09-467-082-3

; Sequence 3, Application US/09467082

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION

; FILE REFERENCE: RTS-0088

; CURRENT APPLICATION NUMBER: US/09/467,082

; CURRENT FILING DATE: 1999-12-17

; NUMBER OF SEQ ID NOS: 49

; SEQ ID NO 3

; LENGTH: 2549

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (81)..(1136)

; NAME/KEY: unsure

; LOCATION: 6

OTHER INFORMATION: unknown
US-09-467-082-3

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Query Match      3.4%; Score 88.4; DB 4; Length 2549;
Best Local Similarity 47.5%; Pred. No. 8.8e-10;
Matches 365; Conservative 0; Mismatches 391; Indels 12; Gaps 3;

QY 177 cagaagtcctccgggtcggttttaacgacatcgagcggaccctgggcaagcacttc 236
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 cagaacacagcccaacttgatcagtttgaacgaatcaagaccctcgacggctcctc 245

QY 237 gcgggtggtgaagctggcgcgagtcagatcaaccaaaacgaggttgcaataaataatt 296
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 gggcggtgtgtgtgtgaacacagaagcgggaaccactatgcattgaagatcctc 305

QY 297 gataaaacagattag---atcaagcaatttggagaatctatcgtgaagttcagctg 353
    ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 gacaacacagaagtggtgtaactgaacgaatcgaaacacacccctgaatgaagaagcgatc 365

QY 354 atgaagcttcctgaacacacacacacataaagctttaccaggtatcgaagaacaaagac 413
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Db 366 ctgcaagctgtcaacttcctcgtccgaactcgaatcgaagttcctcgaagacactca 425

QY 414 atgcttaactcgtcactgaatttgaataaaatggagaagtgttgattatlgacttcc 473
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 426 aaacttaacatggtcagtgaatgagtcgtcccgcggggagatgttctcacactacggcg 485

QY 474 aacggcaccttgatgagaacgaagcgcggaagaagttctgcaaatcctgtcgcgctg 533
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 486 atcggaaggttcagtgagccccaatgccgtttctacgcgcccagatcgttccctgacctt 545

QY 534 gagtactgtacacacacacacacacacacacacacacacacacacacacacacacacac 593
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Db 546 gagtactgtacacacacacacacacacacacacacacacacacacacacacacacacac 605

QY 594 gatggcacatctgacatcaacgctgcagatlttggatttgggaatttcaagaatcagaa 653
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 606 gaccagcaggtcactacattcagtgacagacttcgttcgccaagcgctgaag----- 659

QY 654 gagcctctgtccagctgtgtgtggagcccccgtatgcggccccggaaagcttttgaagg 713
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 660 ggcgcaccttgacactgtgtggacccccctgagtaacctgccccctgaattatccctgagc 719

QY 714 aaggaatgaaagcccccagctgacatctggaacctggtggcgtgtgtgtgtgtgtgtgt 773
    ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 720 aaaggtcaacaagaagc---gtggactgtgtggccctgtgggttcttactatgaatcg 776

QY 774 gtctgaggtctctcctcctcctcgatggcctaactgcgaagcgttgagacagcggtgtg 833
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Db 777 gccgctgtctacccgctcttcttcgcagaccagcccatccagatctatgaagaatcgtc 836

QY 834 gagggcgctctccgcatccctcttctcatgttccaagactgtgagacgtgatccgcgcgc 893
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 837 tcttggaaggtgtccttcccttcccaactcaagctctgacttgaagacactgctgcggaac 896

QY 894 atgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 941
    ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 897 ctccctgaggtgagatctcaccaagcgcttgggaacctcaagaatgtgg 944
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Search completed: March 22, 2002, 13:20:34
Job time: 8972 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 10:46:42 ; Search time 2393.83 Seconds

(without alignments)
11370.505 Million cell updates/sec

Title: US-09-787-559-1

Perfect score: 2533
Sequence: 1 ggcaccgcggtgcgcgcgga.....aaaaaaaaaaaaaaaaaaaaa 2533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: *
1: em_estfun: *
2: em_esthum: *
3: em_estlin: *
4: em_estom: *
5: em_estpl: *
6: em_estda: *
7: em_estro: *
8: em_estov: *
9: em_hlc: *
10: gb_estl: *
11: gb_est2: *
12: gb_hlc: *
13: gb_hlc: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pln: *
18: em_gss_pro: *
19: em_gss_rod: *
20: em_gss_vrt: *
21: em_gss_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544.8	21.5	701	11	BG719047 602699166
2	493.4	19.5	497	10	AM503500 UI-HF-BND
3	344.8	13.6	924	11	BF783804 602109724
4	325	12.8	2411	12	AK017789 MUS muscu
5	298.6	11.8	315	10	BE247296 TCBAP1E40
6	285	11.3	1076	11	BF537120 602048240
7	280.8	11.1	646	11	BF534711 602048240
8	273.8	10.8	439	10	AI466101 VW40H03.Y
9	267.2	10.5	586	10	AV612708 AV612708
10	267	10.5	763	11	BE795309 601586611
11	265.4	10.3	677	11	BE900808 601674532
12	261.6	10.3	435	10	AI528387 u196h01.Y

13	260.8	10.3	866	10	AU132239	AU132239
14	257.4	10.2	748	11	BG825423	BG825423
15	251	9.9	393	11	BF470340	BF470340
16	249.4	9.8	618	10	AM822854	uq20h11.Y
17	244.6	9.7	364	11	BG150724	BG150724
18	244.6	9.7	720	11	BF686388	BF686388
19	244.4	9.6	744	10	AU125196	AU125196
20	241	9.5	995	11	BE798169	BE798169
21	233.8	9.2	810	11	BE901918	BE901918
22	232.4	9.2	836	10	AL538014	AL538014
23	232	9.2	537	11	BG895652	BG895652
24	231.6	9.1	698	10	AI065116	AI065116
25	230.2	9.1	865	10	AU120606	AU120606
26	227.4	9.0	678	11	BF384466	BF384466
27	225.6	8.9	576	10	AW913033	AW913033
28	225	8.9	842	10	AA867040	AA867040
29	223.6	8.8	574	10	BE135068	BE135068
30	222	8.8	264	11	BF914785	BF914785
31	221.8	8.8	530	10	AI115830	AI115830
32	215.4	8.5	518	10	AA633979	AA633979
33	215.2	8.5	753	10	AL037119	AL037119
34	214.4	8.5	545	10	AI108898	AI108898
35	214.4	8.5	2898	12	AK004737	AK004737
36	214	8.4	236	10	BE001845	BE001845
37	213.4	8.4	380	10	BE257296	BE257296
38	211.4	8.4	295	11	BI223469	BI223469
39	211.4	8.3	586	11	BG774205	BG774205
40	207.2	8.2	594	10	AI806648	AI806648
41	204.6	8.1	242	11	BF363385	BF363385
42	201.2	7.9	723	10	AU171067	AU171067
43	200.8	7.9	325	10	AI019741	AI019741
44	200.4	7.9	708	11	BF309150	BF309150
45	200	7.9	674	11	BG976578	BG976578

ALIGNMENTS

RESULT 1
BG719047 701 bp mRNA EST
LOCUS 602699166F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831049 5',
DEFINITION mRNA sequence.
ACCESSION BG719047 GI:13998234
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 701)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10753 row: C column: 18
High quality sequence stop: 701.
Location/Qualifiers
1. 701
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4831049"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"

FEATURES

source

/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 171 a 181 c 217 g 132 t

ORIGIN

Query Match 21.5%; Score 544.8; DB 11; Length 701;
Best Local Similarity 98.4%; Pred. No. 8,2e-67;
Matches 571; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

OY 8 aggtgagcgagagccatgttataatcgtcgaagtcagcgagcccgagccagag 67
|||||
Db 123 AGGTGCGCGGAGCCATGTTATCATGCGAGTTACCGCGGAGCCCGGCGCAG-G 181
68 tcagggcagcagaagcccccctccgggtgggttttaccatcagcgagccctggcga 127
|||||
Db 182 TCAGGGCCAGCAGAGAGCCCTCCGGGTGGTTTTCACATCGAGCGAGCCCTGGGCA 241
OY 128 agcgaacttcggtgtgtaagctggcgcgatcgagtcacaaacgcaagttgcaat 187
|||||
Db 242 AGGCAACTTCGCGGTGGTGAAGCTGGCGCGCATCGACACCAAAACGACAGTTGCAT 301
OY 188 aaaaataatgtataaacaacgaattagatcaacgaattgggaaataatctatcgtgagt 247
|||||
Db 302 AAAAATAATGTATTAACACGATTGATTTCAGCAATTTGGAAATCTATCGTAGGT 361
OY 248 tcagctgtatgaagcttcgaaccatcacacatacgaagcttaccaggtatgtgaac 307
Db 362 TCAGCTGATGAGCTTGTGAACCATCCACATCATTAAGCTTTACAGTATGTGAAC 421
OY 308 aaggaacatgcttataatcgttactgaatgtctaa-aaatggagaatgttgaattat 366
|||||
Db 422 AAGGACATGCTTACATCGTCTACATGAATTTGCTAACAATGGAGAAATGTTGATATT 481
OY 367 tgacttcaacgagcactgagtgagaaacgagcgaggaagaagtcttggcaatccgt 426
Db 482 TGACTTCCACAGCGGACCTGAGTGAACAGAGCGCGGAGAAAGTTCTGGCAATCCGT 541
OY 427 cggccgtgtgagtactgtcaagcaacacatcgttccacgggaacccaagaaccgaacc 486
Db 542 CGGCCGTGGAGTACTGTACGACCATCATCGTCCACCGGAGCTCAAGACCGAGAAC 601
OY 487 tccctcgtatgagcaaatgagatcaagctggcagatcttggatttggaaattctaca 546
Db 602 TCCTCTGATGAGCAACATGACATCAAGCTGGCAAGATTTCGGAAATTTCTACA 661
OY 547 agtcagagagacctctgtccacgtgtgttgaggagccccc 586
Db 662 AGTCAGAGAGCCTCTGTCCACGTGTGTGGAGCCCCC 701

RESULT 2
AM503500 497 bp mRNA EST 01-MAR-2000
LOCUS UI-HF-BNO-aic-g-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION IMAGE:3079113 5', mRNA sequence.
ACCESSION AM503500
VERSION AM503500.1 GI:7140059
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 497)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
EMAIL: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
SOURCE Location/Qualifiers

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/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Ronaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 75 a 180 c 160 g 82 t

ORIGIN

Query Match 19.5%; Score 493.4; DB 10; Length 497;
Best Local Similarity 99.8%; Pred. No. 1.3e-59;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1232 cgaagtgaactgtagctcagagctcgtcgaatgagccctgtcttcccgatgagtc 1291
Db 3 CGAGGTGACGTGAGCTCAGAGCTCGCTGCAATGGCCCTTGTCTCCCGGTGATGC 62
OY 1292 cagcttgacgaggaatgttctcggcccgcccgctgttcccaagacgctgtcgaacagc 1351
Db 63 CAGCTGACGCGAGAGTTCGCGCCCGCCGCTGTCCCAAGCAGCAGCTGTGACACAGC 122
OY 1352 catcagtgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1411
Db 123 CATCAGTGAGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182
OY 1412 cctgccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1471
Db 183 CCTGCCAGCAGCAGCGGCGGAGGAGCAGACCTGTGCGAGAGTTCACACCGCCTC 242
OY 1472 actaacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1531
Db 243 ACTACCGCGCCAGTATGATGCTGCTCCCTCCACACGCAAGTCTTCAAGAGGAAAC 302
OY 1532 caagcttgacagtgatgtcgaacctctctcgaagcaaaagcccgagcagcagcagc 1591
Db 303 CAGCTTGACAGAGTGTGTGACCTCTCTGCGAGCAAAAGCCCGCGGAGCTCAGTGG 362
OY 1592 cccgggcaactcaggggtgtgtggcgctgtcctcccgatgaagcgtgagcctgctcct 1651
Db 363 CCGGCGCAGTCAGGGGTGTGGGCGGCTCTCCCGGTGAGCTGGCCCTCCCTCC 422
OY 1652 ggggtcgaatccgcaaccccaagtgatcgaagcagcagcagcagcagcagcagcagc 1711
Db 423 GGGGTGCAATCCGCCACCCCACTGCTGAGGCTCAGAGGGGCTTGGAGAGAGCTGTCT 482
OY 1712 gctccctgtcagctt 1726
Db 483 GCTCCGTGACGCTT 497

RESULT 3

Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, Y., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES
source
Location/Qualifiers

1. 2411
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="MGD:MGI:1903082"
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2393..2398
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2411
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BASE COUNT
606 a 610 c 627 g 568 t
ORIGIN

Query Match 12.8%; Score 325; DB 12; Length 2411;
Best Local Similarity 61.2%; Pred. No. 1.7e-36;
Matches 545; Conservative 0; Mismatches 340; Indels 6; Gaps 1;

QY 183 gcaataaaataatgataaaacagatagattcaagcaatttggagaaatctatcgt 242
DB 65 ggaacaaactgcagctttaaagccagctgtagaagaaactttaaagcttccgg 124
QY 243 gagctcagcgtgaatgaacttcctgaacatcacacatcataaagcttaccagttatg 302
DB 125 GAGGTTCAGATATGAAATGCTTTGCCATCCACATCATCAGACTTACCAGGTCATG 184
QY 303 gaacaaagacatgcttaccatgctcactgaattgtctaaatgagagaattgttcat 362
DB 185 GAGACAGAGCGCATGATTACCTGTGACAGATACGCTAGCGGAGAGATATTGAC 244
QY 363 taattgactccaacgacactgagtgagagaagcgcggaagaattcttgcgaatc 422
DB 245 CACTTGTAGCCCATGAGATGACAGAGAAAGCTCCACGGAAGTCAAAACAGATC 304
QY 423 ctgtcgcctggtgagtgactgtcagacatcacatcgtccacccggaactcaagccgag 482
DB 305 GTCAACAGCGGTGATTGTTGCTACTGCTGGAATATCGTTCAATCGTATTTAAACCGGAA 364

QY 483 aacctccctgtagatgtagcaacatgacatcaagctgagatatttgatttgggaatttc 542
DB 365 AACTTACTTTCGGAGGCCAATCTGATATCAAAATAGACAGACTTTGGCTTCAGAACCTC 424
QY 543 taacagtaagaagagactcttccacgtgtgtgtgtggagagcccgatgacgcccggaa 602
DB 425 TTCACTCCAGGCGACCTCTCAAGACGTCGTGTGACACCTCTCCATTAGCCGCCCAAG 484
QY 603 gtctttagagaaagagtagtgaagagcccccagcagcagcagcagcagcagcagcagc 662
DB 485 CTCCTTGAAGGAGAGAAATATGATGAGGCCCCAAAGTGGCATATGAGCTTGAGCTTTC 544
QY 663 ctgtacgtcctgtgtcgtgtcctcctcccttcgtagtggcctaaactgcgacgctgaga 722
DB 545 CTCTATGTGCTGTGTGTGTGGCCCTGCGCTTGTATGGAGACACATCGACAAATCTGCG 604
QY 723 cagcgggtgtcgtgagagcgcttcgcgaatcccccttcacatgctcaagactgtgagagc 782
DB 605 GCCCGCGTGTGAGTGGAGGAGTTCGCGATCCCGTCTTATGTCCACAGAGTGTGAGCAG 664
QY 783 ctgacgcgcgcgcatgtgtgtgtgtgagcccgccagcgcatcacatgcgcccagctcg 842
DB 665 TTGATCCCGCCACATGCTGTGTGTATGATCAATAAGCCCTCTCATATGAACAGATCTGC 724
QY 843 cagcacccgtgtgatg-----cgggtgagccctgtgtgtccgggacccgcctgcccgc 896
DB 725 AGGCACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
QY 897 ttctcgcacacagcttaacactccacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 956
DB 785 TGCCAGCACTGAAAGAGAGAAAGGAGTGGAGACCCCTCAACAGATGATGATGATGATG 844
QY 957 atcgagaccctgt 1016
DB 845 ATGGAAGACATGCGGCTGTGACAGAGCGCACACTTCACTGATTAAGTCAAGTCAAGTCA 904
QY 1017 aaccactgt 1067
DB 905 GACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

RESULT 5
BE247296
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BE247296 315 bp mRNA EST 15-NOV-2000
TCBAP1E4075 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC Project-TCBA Homo sapiens cDNA clone TCBAP4075, mRNA
sequence.
BE247296
BE247296.1 GI:9099050
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 315)
Wei, Y., Tsang, Y.-T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric leukemia cDNA sequencing Project
Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Seq primer: M13 primer
Location/Qualifiers
1. 315
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP4075"
/clone_id="pediatric pre-B cell acute lymphoblastic

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leukemia Baylor-HGSC project-TCBA
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
```

/note-vector: lambda psb, site_1: BamHI; site_2: EcoRI;
 First strand cDNA was primed with an anchored
 XhoI-oligo(dT) primer [5'GCGAGCTCGGCGCCGAGAGAG(T)VN
 3']-Va-C-G-N-A-C-G-[n] and then dg tailed. Second
 strand was primed with a BamHI-dC primer
 [5'AGAGAGCTCGGATCGCGGCGCGCAATATATATAT(C) 3'].
 Double-stranded cDNA was then digested with BamHI and
 XhoI and directionally cloned into the BamHI and SalI
 sites of lambda psb vector. Library went through one
 round of normalization. Library was constructed by Wel

BASE COUNT	55 a	106 c	98 g	56 e
ORIGIN				

Query Match	11.8%	Score 298.6	DB 10	Length 315
Best Local Similarity	97.1%	Pred. No. 1,8e-32		
Matches 304; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

QY	835	agatccgacagacacggtgatgtcgggcttagcccttgatccggtgacccgcttcgccc	894
Db	1	AGATCCGGCAGACACCGGTGATCGGGGCTGAGCCCTTGCCGGGACCCGCTGCCCG	60
QY	895	cccttcctcgacaacagctaaacctccaaccttgggcactcagatgacagcgctggtta	954
Db	61	CCCTTCCTCGACACAGGTACTCTCTTAACCTGGGGCAGCTACGATGAGACAGCGCTGGTA	120
QY	955	tcatgacagacccttgggcgcttgagaccgacgacgagacggttgagctacgtcaaaacagcagt	1011
Db	121	TGATGACAGACCCGTGGGTGTGGACCGGAGAGGACGGGGAGTCACTGCAAAACAGCAGCT	180
QY	1015	ataaacacttgcgtgcattatatacctcctccttgaagcggtccaaagagatatacgaaatg	107
Db	181	ATAAACCCCTTTGCTGCGCATTATTATTAACCTCTCCCTTGAGCGGCTCAAGAGACTATCGGAATG	240
QY	1075	cccaagtcagccgcgccccgggacctgacagagcagcccgagccttcggaagctcagaaactcaatg	113
Db	241	CCGAGTGCGCCGCCGCCGCCGCGCTGCGAGGACAGCCGGGGCTTCGGAGCTCGGACCTCAATG	300
QY	1135	gtttggaagtgtcc 1147	
Db	301	gTTTGGAGGGGC 313	

RESULT	6
BFS37120	
LOCUS	BFS37120
DEFINITION	602049032F1 NCI_CGAP_SG2 Mus musculus cdna clone IMAGE:418835 5'
ACCESSION	BFS37120
VERSION	BFS37120.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
REFERENCE	1 (bases 1 to 1076)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAW512 row: p column: 08
High quality sequence stop: 712.
location/Qualifiers
1..1076

```

BASE COUNT	301 a	256 c	342 g	177 t
ORIGIN				

Query Match	11.3%	Score 285;	DB 11;	Length 1076;
Best Local Similarity	66.3%	Pred. No. 8.6e-31;		
Matches 425;	Conservative	0;	Mismatches 215;	Indels 1;
				Gaps 1

OY	217	caagcaaatctgggaaatatctacgcggaagttcaagctctgaagcttcgaaacca-tcca	275
Db	1	CCAGTACTCTGCAGAAGCTGTTCCAGGAAGTCCGAAATTATGAAGGACATCAACACC	60
OY	276	caacataaagctttaccaggltatggaacaagaagacatgcttatactgctactgaa	335
Db	61	AGCATCTGTGAAGCTTTTGGTGTGAATGAGACCGAACAACCGTATTAACCTGGTGTG	120
OY	336	tttgcataaaatggagaatagtttggattttatcttgaacttccaaacgggagacgtgtagaac	395
Db	121	TACGCTTAGCCGAGGAGAGAGTGTTCACCTACCTCTGTTCCACGCGCCGATGAAGGANA	180
OY	396	gaagcgaggaagaagttcttgcacaatccctgctcgccggtgagtagtaactgacagcaatcac	455
Db	181	GAGCGTCGAGCCAAAGTTCCGGAGATCGTGTACGCCGTGCACACTGATCATCAAGAAG	240
OY	456	atcgctcaaccgggaactcgaagaccgggaacccctctcgtgtatggtgcaaatgagatcaag	515
Db	241	ATTGTACACAGGGATCTTAAAGGCTGAAACCTGTTCTGATGATCCGACGCCAATCAAA	300
OY	516	cttgcagaaatttgatttggaaatttctcacaagtcaagagagacctctgtccacgtcggtgt	575
Db	301	ATCGCGCACTTCGGCTTCAGCAATGAGATTGACGCTGGGCTCCAAGTGGACACCTTCTGT	360
OY	576	ggagagcccccgatagtcgcgcgcccggaagctcttgaaggaaagatataagagccccca	635
Db	361	GGGAGCCCCCATATGAGCGCCGCCAGAGAGCTGTTCCAAGGCAAGAATGATGATGGCCAG	420
OY	636	cttgaacatctggagaccttggcgctggtgctgctgaagctccgtgctctgctgctctccctc	695
Db	421	GTTGAGACATTCGAGGCCCGGGGTGTATCTCTGTATACATCGCTGATACGCGCTCCCTG	480
OY	696	gatggagctaacctgcgcagcgtctgagacagcgggtctgtggaaggccgctcttcgcatccc	755
Db	481	GATGGGACAAACCTCAAGGAGCTGCGGGAGACGAGTCTCTCAAGAGAAATGATACCGGGGTCC	540
OY	756	tctctcatctcagaagactgtgagagccttgatctcgcgcgaatgctgtgtgtgtgagaccgc	815
Db	541	TTTCTACATGTCGTACAGACTGCGAGACATTTCTTCGGAGATTTTCTGTGCTGTGAACCCGCA	600
OY	816	aggcgcatcacatcgcccaagatctcgagcagcagccggtgat	856
Db	601	AAACGCTGTACTGGAGCAAAATCATGAAGAACAATGTGAT	641

RESULT	7				
LOCUS	BF534711				
DEFINITION	BF534711	646 bp	mRNA	EST	11-DEC-2000
	602048240F1	NCI_CCAP_SG2	Mus musculus	cdna clone	IMAGE:4187769 5'

	ACCESSION	mRNA sequence.
	VERSION	BF534711
	KEYWORDS	BF534711.1 GI:11622074
	SOURCE	EST.
	ORGANISM	house mouse. Mus musculus Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
	REFERENCE	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
	TITLE	Unpublished (1999)
	JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cga@bs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNI at: http://image.llnl.gov Plate: LHAM9510 row: p column: 10 High quality sequence step: 646.
	FEATURES	Location/Qualifiers
	Source	.646 "/organism="Mus musculus" /strain="FWB/N" /db_xref="taxon:10090" /clone="IMAGE:4187769" /clone_1kb="NCI_CGAP_SG2" /lab_host="DH10B (TI phage-resistant)" /note="Organ: salivary gland; Vector: pcMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
	BASE COUNT	172 a 153 c 178 g 143 t
	ORIGIN	
Query Match	11.1%;	Score 280.8; DB 11; Length 646;
Best Local Similarity	67.6%;	Pred. NO. 4.1e-30;
Matches 438:	Conservative 0;	Mismatches 207; Indels 3; Gaps 3;
OY	73 gccagcagaagcccttcgggtggttttaccacatcgagcgcgaccttgycacaagca	132
Dd	1 GGGGTCGTAGTGCCCTCGCATCGCTACTTAGAATCACCACGCCACATCGCAAGGGA	60
OY	133 acttcgcgggtgttgtagactcgcgcgcgcgatcgcgagtccaaccaacgcgaaggctgcatanaaa	192
Dd	61 ACTTCGCTGTGTTCAAGCGCGCCAGCACACTTGTCACCAAGGCCAAAGTTCATTATAAA	120
OY	193 taattgataaaaaacagattagattcaagaatttggagaaa-aactatcgttaggtcaa	251
Dd	121 TCATGATTAAGAAGCCAGCATGTAAGAAAACCTTAAGAAGATGTGTCGGAGAGTTCAG	180
OY	252 ctgataagaactctgaacacatcacacatcataaagctttaccaggtltaagaaacaag	311
Dd	181 ATAATGAAGATGCT-TGCCATCCACATCATCAAGACTTACCAGGTCTGAGACAGNG	239
OY	312 gaacatcttiaaatcgtcaactgaatttgcataaaaaatggagaatlttgtatatlttgact	371
Dd	240 CGCATGATTACTCTGGTGCACAGATNCGCTACGCGAGGGAGATATTTTGACCACATTGGNA	299
OY	372 tcacaagcggcactctgaagtgaagaagcggcggaagaagttcttgcgcaatcctctgcgcc	431
Dd	300 GCCCATGTGAAGAATGGACAAGAACGAAGCTTCACAGCAAATTTTAAACAGATCTCACACGC	359
OY	432 gtgcggaactctgacagaacatcacatcgtctccacgcggacctaacagaacgcgaacctctg	491
Dd	360 GTGATTTTTTGTCACCTGTCGGAATATCGTTACCTGATTTAAAAACGCAAAACTTACTT	419
OY	492 ctggaatgacaacatgacatcaacgtcgcagatlitggatlitggaaatttcttacaaagta	551

Db	420	CTGGACGGCAATCTGAATATCAAAATATACAGACTTTGGCTTCAGCAACCTTCACCTCA	479
QY	552	ggagagcctctgtccacgtgtgtgtgtggagccccccgtatgtcgcgccccgggaagctttgag	611
Db	480	GG-CAGATGCTGAAGACGGTGGTGGCAGCCCTCCCTATGCGGCCCCAGACTCTTGAA	538
QY	612	gggaagagatgaagagccccccagcttgacatctgaagacctgggctgtgtctgaagtc	671
Db	539	GGGAAGGAATATGATGAGGGCCCAAAATGGACATATGACACTTGGATGCTCCTATGTG	598
QY	672	ctgtctctgcggtctctctccctctgagtgcctaacctgcgcgaagctg	719
Db	599	CTGGTGTGTGGCGCCCTGCCCTTGGATGGAGACACACACACAGAAATCTG	646
RESULT	8		
LOCUS	A1466101	439 bp	mRNA
DEFINITION	v440h03.y1	Soares_mammary_gland_NbMWG	Mus musculus cDNA clone
ACCESSION	IMAGE:1246325	5'	similar to SW:MSK_MOUSE_060670 PUTATIVE
KEYWORDS	SEKINE/TREONINE-PROTEIN KINASE MSK ;		mRNA sequence.
REFERENCE	A1466101		
AUTHORS	A1466101.1	GI:4320131	
TITLE	EST.		
ORGANISM	house mouse.		
SOURCE	Mus musculus		
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
COMMENT	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 439)		
	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-rtmail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MG1:660013		
FEATURES			
source			
	This read is a RESEQUENCE of a previously sequenced mouse clone		
	This read has been verified (found to hit its original self in the		
	correct orientation)		
	Seq primer: -40RP from Gibco		
	High quality sequence stop: 380.		
	Location/Qualifiers		
	1..439		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:1246325"		
	/clone_lib="Soares_mammary_gland_NbMWG"		
	/sex="male"		
	/tissue_type="mammary_gland"		
	/dev_stage="4 weeks"		
	/lab_host="DH10B"		
	/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia		
) with a modified polylinker; Site.1: Not I; Site.2: Eco		
	RI; 1st strand cDNA was primed with a Not I - oligo(dT)		
	primer 15'		
	TGTTTACCATCTGAAGTGGGAGCGCGCCGCGAATGCTTTT		
	T 3'] : double-stranded cDNA was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pT7T3 vector.		
	RNA provided by Dr. Minoru Ko, Wayne State Univ. Library		
	constructed and normalized by Bento Soares and M.Fatima		
	Bonaldo."		
BASE COUNT	87 a	157 c	107 g
ORIGIN			88 t
Query Match	10.8%	Score 273.8	DB 10; Length 439;
Best Local Similarity	78.3%	Pred. No. 4.4e-29;	
Matches 342; Conservative	0;	Mismatches 92;	Indels 3; Gaps 1;

QY	1110	cgagctctggagctcggagctcagctggttttgagaggtgcctcagaaggtctcttcacacgc	1169
Db	5	CAGCTCCGAAAGCTCAGACACTCAGCAGTCTGGAGTTCTTCAAGAAATTTCTCCCTGTGTGAC	64
QY	1170	cccttcgcagctctgctctgtgtcccgccagccgcagacctgtgtgcagctcgtctccag	1229
Db	65	CTTTTTCGCGCCCTCTCTGCTGTGGCCACAGCCCAAGGCTTGGCTCAGTCTGCTCTGGAG	124
QY	1230	ggcagagatgactgttgagctccagagctcgtctgcagtggtggtcttctccggttgat	1289
Db	125	GCTGGATAGACTGTGATCTCCACAGCTCACACTCA---GCCCTATTATTCTCCCTGTGAT	181
QY	1290	ggcagctcgcagcggagtggtctgcggccggccggcggtgtgtcccaagagctgtgtgacaca	1349
Db	182	ACCAACTCAGAGGGAGTGTCTCCGGACCGATTCATCTCCCAAGCAGTCTGCTGGACACA	241
QY	1350	ggcatcagtgaggaagcagagcagagggccgggacctagaggaagagagacacagcagag	1409
Db	242	GCTATACACGAGAGAGCCAGCGAGGTCTCCAGGCTATATAGAGAAACAGSAGGTCCAGAA	301
QY	1410	tcacctccagcagcagcggcgccggagacacacctgycgcagtggtctccaccgcctctcc	1469
Db	302	CCCCGCCCCGAGACAGCGCGGAGGACACATATGGCTGAGTCTCCACCATTTCTCC	361
QY	1470	ccactccacggcgcaatgatatgtgtctccctccaccacagcgaagtctctcagaagga	1529
Db	362	CGCTCAACCCCTCTTGATATTGTCTCTCTGTCCGACGCGGACGTCCTCGGAAGAGG	421
QY	1530	accagctctgcagctgtg	1546
Db	422	ACCACTCTCCGACAGCTG	438
RESULT	9		
LOCUS	AV612708	586 bp	mRNA
DEFINITION	AV612708 Bos taurus lung fetus Bos taurus cDNA clone E11U047B05 5',	EST	30-AUG-2000
ACCESSION	AV612708		
VERSION	AV612708.1	GI:9748378	
KEYWORDS	EST.		
SOURCE	ccv.		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovidae; Bovinae; Bos.		
	1 (bases 1 to 586)		
	Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Itohzono, A. and		
	Suzuki, H.		
TITLE	bovine cDNA sequencing		
JOURNAL	unpublished (2000)		
COMMENT	Contact: Yoshikazu Sugimoto		
	Animal Genetics Institute		
	Shirakawa Institute of Animal Genetics		
	Odakura, Nishigo, Nishi-Shirakawa, Fukushima 961-8061, Japan		
	Tel: 81-248-25-5641		
	Fax: 81-248-25-5725		
	Email: kazusugi@ccoa.ocn.ne.jp		
	Single pass sequencing		
FEATURES	This clone was obtained from a polyA-deleted cDNA library.		
SOURCE	Location/Qualifiers		
	1..586		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/clone="E11U047B05"		
	/clone_lib="Bos taurus lung fetus"		
	/tissue_type="lung"		
	/tissue_type="fetus"		
	/dev_stage="fetus"		
	/lab_host="DH10B"		
	/note="Vector: pZLI; Site1: SalI; Site2: NotI; Poly A		
	was deleted from a NotI site"		
BASE COUNT	135 a 143 c 165 g 143 t		
ORIGIN			

Query Match	10.5%	Score 267.2	DB 10	Length 586
Best Local Similarity	67.8%	Pred. No. 3.3e-28		
Matches 388	Conservative 0	Mismatches 183	Indels 1	Gaps 1
QY 287	gctttaccaggltatlgaaacaagagatcgtcttacatcgtcactgtgaattgtccta	aa	346	
Db 12	gctttaccaggltatlgaaacaagagatcgtcttacatcgtcactgtgaattgtccta	aa	71	
QY 347	tggaggaatgtgttgatatttgacttgcattccaaggcaccctgtgtgaaacggggc	gaa	406	
Db 72	aggggaattatttggaccacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	g	131	
QY 407	gaattctcggagaaatcccgctcggccgttgagtaactgtacagcaaccatcgtcc	ac	466	
Db 132	caagttcaaacagatcgtgttgacgacgctgtattttttgtcagtgtggaaatgt	gttcac	191	
QY 467	ggaacctcaagacggaaacctcctgtctgtatgtgcaacatgtgacatcaagctg	gcaatt	526	
Db 192	tgatttttaaacctgtaaaatttgcctcttgacgaccccaatgtgaatttcaaga	tatgcagatt	251	
QY 527	tgatttttgagaattctctcaagtcagagagacccctctcagcgtgtgtgtggag	cccccc	586	
Db 252	tgagcttcagtaacctcttaccacccctggcagactactgaagacctgtgtgtg	cagaccttc	311	
QY 587	gtatgcgccccggaaagctcttgaaaggaaagagatataaaggccccacgtga	catctg	646	
Db 312	ctatgctcctctcgtaaccttttgaagaaagagatgacgaccccaaggtgacat	ctg	371	
QY 647	gagccttgagcgtgtgtgtcgtactgtcgtgtgtgtgtgtgtgtgtgtgtgtgt	gt	706	
Db 372	gagccttgagcgtgtgtgtcgtactgtcgtgtgtgtgtgtgtgtgtgtgtgtgt	gt	431	
QY 707	ctgtcgcgagcgttgaaacagcggtgtcgtgaaggcgccgtccgcacatccctc	atcatgtc	766	
Db 432	actgcagaaatctgcgcggccgggtgtgtgaaggaaatttgacatccatttttat	gttc	491	
QY 767	tcaagactgtgagagcctgtatccgcgcgcatgtcgtgtg-tggaaacccgca	ggcgatca	825	
Db 492	cacagaaatgtgagcaccctgtatccgcgcgcctgtgtgtgtgtgtgtgtgtgt	gt	551	
QY 826	ccatgcgccagatccgcgagcagcagcgtgtgtgtgtgtgtgtgtgtgtgtgt	gt	857	
Db 552	tcattgacacagatctgcacaaagcccaagatgtgtgtgtgtgtgtgtgtgtgt	gt	583	
RESULT 10				
BE795309	763 bp	mRNA	EST	20-SEP-2000
LOCUS	601586611F1 NIH_MGC_7	Homo sapiens	CDNA clone	IMAGE:3940970 5'
DEFINITION	mRNA sequence.			
ACCESSION	BE795309			
VERSION	BE795309.1	GI:10216507		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
DATE	1 (bases 1 to 763)			
FILE	NIH-MGC http://mgs.nci.nih.gov/			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: DCTD/DRP			
	CDNA Library Preparation: Ling Hong/Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov			
	Plate: LNCM/92 row: e column: 03			
	High quality sequence stop: 551.			

Db	241	TGTCGCGATTCACTACTGGCATTACGAAAGGATCTGTAACATCGAGACTCAAGGCTGAAA	300
QY	484	accctccgctgagatgagcaacatgacatcaagctgcagatlttgatlttggaaatttct	543
Db	301	ATCTATTGTTAGATGCGGATATGAACTTTAAATATGCAAGATTTTCGTTTATGCAATGAAT	360
QY	544	acaaatgaagaaagcctctctgccagctgctgctgagagccccgatalgcgcgcccgaaag	603
Db	361	TTACTGTTGGCGGTAATCTGACACGCTTTGCTGGCNACTCTCCATACGACGACCTGAGC	420
QY	604	tctttgaagggaaagaglatgaagcccccaagctgacatctgagacctgagcctgctgctgc	663
Db	421	TCTTCCAGGGCAAAATATGACGGCGGACGAAAGGATGTGTGAGTCTGGGGTCAATT	480
QY	664	tgtacgtccctggtctgcggtctctctcccttcgatgtgagcctaactgcagctgagac	723
Db	481	TATACACACTGATCTAGTACGTGGCTCACTTCCCTTCGATGGGCAAAACCTTAAAGAACTGAG	540
QY	724	agcgagtgctcgagaaaggccgctctccgcatccctctctcatgctctcaagacttgagagcc	783
Db	541	AGAAAGATATCAGAGGGCAATATCCGAATTCCTCTTACATGTCTACGACTGTGAATAAC	600
QY	784	tgaatccgcgcgatgctggtgtagaccgcgcagcgagcatcacacatctgcccagatccgc	843
Db	601	TTTCTCAAACTGTTCTCTGCTGCTAAATCAATTAAACGCGGCTACTTATAGACCAATCATGA	660
QY	844	agcacgcgtgagatgc	858
Db	661	AGGACAGGTGATCC	675

RESULT	12
LOCUS	A1528387
DEFINITION	A1528387 435 bp mRNA EST 18-MAR-1999
ACCESSION	U196H01.Y1 Sugano mouse liver mla Mus musculus cDNA clone
VERSION	IMAGE:1990289.5', mRNA sequence.
SOURCE	A1528387 A1528387.1 GI:4442522
ORGANISM	EST. house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus- 1 (bases 1 to 435)
AUTHORS	Marrer,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,R., Steptoe,B., Theising,B., Allen,M., Bowers,Y., Pearson, B., Swaller,K., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter, .E., Koln,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson.R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 266 1800 Fax: 314 266 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:974613 Seq primer: custom primer used High quality sequence stop: 429. Location/Qualifiers 1..435
FEATURES	
source	

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location/Qualifiers
1..435
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890289"
/clone_lib="Sugano mouse liver ml1a"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
note=Organ: liver; Vector: pME18S-FU3; Site_1: DnaIII
```

(CACTGCTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dt) primer [ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCCTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGCTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTTAAGCTGCG and 3' end primer CGAAGCTGACGTCGACACA."

	Query Match	Similarity	10.3%	Score	261.6	DB	10	Length	435
	Best Local	Similarity	76.6%	Pred.	No. 2.2e-27				
	Matches	334	Conservative	0	Mismatches	99	Indels	3	Gaps
OY	1492	tcgtctcccccctcaccacacagcgcaagtccctgcacagaggaaacacgactgcgaattgtctga	1551						
Dd	2	TTGTCTCCTCTGTCGCCACGGCGAGTCCCTCGGAAGGAGCACAGCTCCGACGCTGCCTCC	61						
OY	1552	ccttctctgcggagccaagaagccccgcgggggtctaagtgcacccccgcacctcacggggctgc	1611						
Dd	62	CCTTCCTGCAAGTAAAGTCTCCGACAGGCGCTTGCGACGTGGCCCTGGCCACCACAGGGCTCC	121						
OY	1612	tgggagcctgtcccccggatcgaagcttgagctcgccctctctctgtgggtgtcgcagtcgccacc	1671						
Dd	122	TGGGACACCAAGCTCTCCAGTCCAGATATTGGCTCCGCCCTTCCTGGGATTCACAGTCAAGCCACC	181						
OY	1672	cagtgctgcgaagctcgaagggggtcttggaagagagctgttgtcctccctgcagttccag	1731						
Dd	182	CTGTCTCTCCAGACTGACGACGCTGTGGCGACACCGCTTTACTCTCCGCTCAGGCTTTCAGG	241						
OY	1732	aggagcgcgcgggcgtctgcagacaccttaactgacctcaagggtctgaaggccttgcggcagcagc	1791						
Dd	242	AAGGACGGAGACGCTGTGTACTCTCTCTACTCAAGGGCTTGAAGGCTTCCGGACACAC	301						
OY	1792	tgaagaaagacccacgcggagcaaaagggttcttgtagactgacaataacaaagggtctgc	1851						
Dd	302	TGAGGAAAAAATGTCGAGGACCAAGAGGGGTTCTGTGGACTGAACAAGATCAAAGGGTTGGCTC	361						
OY	1852	gtccaggtgtgcgaagttccctgcacgcgggccaagcaggggcggtctgaagcccttccaa	1911						
Dd	362	GCCAGGTTGTGCCAG--TCTCTCCGTTCCGAATCCCCGGGGAGGATGAATACTTTCACA	418						
OY	1912	ccccgtcacagagagccc	1927						
Dd	419	CCCCAGCCCCCAAGCTC	434						
RESULT	13								
AUI32239									
LOCUS	AUI32239	866 bp	mRNA	EST	24-OCT-2000				
DEFINITION	AUI32239	NT2RNP3	Homo sapiens	CDNA clone	NT2RNP3004052 5'				
ACCESSION	AUI32239								
VERSION	AUI32239.1	GI:10992593							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE	1 (bases 1 to 866)								
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.								
TITLE	HRI human CDNA project								
JOURNAL	Unpublished (2000)								
COMMENT	Contact: Takao Isogai Genomics Laboratory								

LOCUS	BG825423	748 bp	mRNA	EST	22-MAY-2001
DEFINITION	602746835F2 NIH_MGC_17		Homo sapiens	cdna	IMAGE:4959824 5'
ACCESSION	BG825423				

VERSION	BG825423.1	GI:14173010
KEYWORDS	EST.	

SOURCE	human.
ORGANISM	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 748)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgabbs-remail.nih.gov

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1792 row: e column: 09
High quality sequence stop: 746.

FEATURES	Location/Qualifiers
source	1. .748

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/organism="Homo sapiens"  
/db xref="taxon:9606"
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/clone-"IMAGE:4899824"  
/clone_11b-"N1H MGC 17"
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/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"

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/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming."

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directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGCG (Size-selected >500bp

for average insert size 1.8kb. Library constructed by

ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Eurotranscript II DM (1450 nucleotides) [1].

(Stralageme) and superscript II KI (late reclinologies).

BASE COUNT	222 a	163 c	182 g	181 t
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ORIGIN

Query Match 10.28; Score 257.4; DB 11; Length 748;

Best Local Similarity 61.3%; Pred. NO. 6.8e-27;
Matches 448; Conservative 0; Mismatches 281; Indels 2; Gaps

116 gaacctgggcaagaagcaacttcgcgylgltgaagctggcgcgycatcgagtcaccaaacc 175

Db 14 GACCATGGCAAGGTAATTTTGCAGGTGAAGTTGGCCCGCACACATCCGACTGGGA 73

QY 176 qcaggttgcataaataattgataaacaacgattagattcaagcaatttgagaaat 235

Db 74 AGAGGTAGCTGTGAGATCATTTGACACAGACTCAACTGACTCTCTCCAGCCTCCAGAACT 133

236 ctatcgtgaagccttcaactgaatgaagccttctgaascacacacatcataaaccttacc 295

Db 1 34 ATTCGGAGTAAAGTAATGAAGTTTGAAGCATCCACATAGTTAAATTATTGCA 193

206 atttatgaaacaaagaaacatcattacatcattgacatcattgacaaatgaaat 355

[illegible][illegible][illegible]

```

OY 416 gcaatctctgagcgctgagatctcagcaccatcactcgtccagcgagactca 475
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DB 314 CCAATAGTGTCTGCTGCTGACGACTGTCACCAAGCTTATTTGTCATAGACTTAA 373
OY 476 gaccgaacactctctgctgagtcacacatgacacagctgacagatttgattgg 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 GCGAGAAACCTGCTCTTGATGCTGATATGACATCAAGATTGACACTTTGGCTTCAG 433
OY 536 gaattctacaagtcagagagacactctgtccagctgtgtgagagaccctcgtatgcgc 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 434 CAATGATATTCACCTTTGGGAACAAGCTGGACACCTTCTGTGGCAGTCCCTTATGCTGC 493
OY 596 ccggaagctcttgagg-ggaagagatagaaagcccccagctgacatctgagccttg 654
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DB 494 CCCGAACCTCTCCAGCAAAAAAATATGATGACCCGAGGTGATGTGGAGCCTTACG 553
OY 655 gctggtgctgtagctgctgctgctgctgctc-ccccctgagtgcccaactcgcg 713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 554 GAGTTATCTCTTATACACTGTCAGCGATCCCTGGCTTTTGATGACAGACCTTCAAG 613
OY 714 acgttgagacagcggtgctgagagcgctcctccatccctctcatgtctcaagac 773
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 614 GAGCTGGGGGACGGGACTAGAGGGAANAATACCGTATTCATCTTACATGTCACGAC 673
OY 774 tctgagagcctgacccgagcagctgctgtgtgtgagcccgccagcgcatcaccatcgcc 833
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 674 TGTGAACACCTGCTTAAAGAAATTTCTCATTTCTTATCCACAGAGAGGACATTAAAGAG 733
OY 834 cagatccgcgca 844
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DB 734 CAAATCATGA 744

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RESULT 15
BF470340
LOCUS BF470340 393 bp mRNA EST 04-DEC-2000
DEFINITION UI-M-BH3-aux-c-08-0-UI.r1 NIH_BMAP_M_S4 Mus musculus cDNA clone
ACCESSION BF470340
VERSION BF470340.1 GI:11539523
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 393)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chih, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestremail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clome distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.

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FEATURES

Location/Qualifiers

1..393

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BH3-aux-c-08-0-UI"

/clone_11b="NIH_BMAP_M_S4"

```

/dev_stage="27-37 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
BASE COUNT 78 a 140 c 93 g 82 t
ORIGIN

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Query Match 9.9%; Score 251; DB 11; Length 393;
Best Local Similarity 79.0%; Pred. No. 6.8e-26;
Matches 312; Conservative 0; Mismatches 80; Indels 3; Gaps 1;
OY 1116 cgaagctcgacacccagtcgagtgctgagagtcctcagaagctctccacgacccttc 1175
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DB 2 CGAAGCTCAGACCTCAGACCTGAGAGGTTCTCAAGAAATTCCTCCGTGACCTTTC 61
OY 1176 cgaactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 CGGCCCTCTCTGCTGTGCTGCCACAGCCCGGCTTGGCTCAGTGTCTGCTCAGAGCTAG 121
OY 1236 atggaactgagcccaagagctgctgagctgctgctgctgctgctgctgctgctgctg 1295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 ATGACTGTGATCTCCACAGCTCACTTCA---GCCCTATTATTTCCCTGGATACCAAC 178
OY 1296 tgcagcgagtgcttcgagcccgccgctgtcccaagcagcctgctgagacagccatc 1335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 TGCAGTGGAGGTTCGCGCACCATTCATCTCCCGACAGCATGCTGGACAGCTATTC 238
OY 1356 agtgaagagagccagagcgagcgagccttagaagagagagagagagagagagagctctg 1415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 AGCAGAGGAGGCGCAGGAGGCTCCAGCCTTAGAGAGAGAGAGCTCAGAGAACCCCTG 298
OY 1416 ccagacagacgagcgagagagacacccctgagcagagctcaccacgctcctcccaatc 1475
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DB 299 CCCGGAAGCAGAGCGGAGGACACATTTGGCTGAAGCTCCACCATTTCTCCCGCTC 358
OY 1476 accgagcagatgatagtcgtctccctccacacac 1510
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DB 359 AACCTCTTGCATTAATTTGCTCTCTCTCCCTCCAC 393

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Search completed: March 22, 2002, 12:14:54

Job time: 5292 sec

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QY 117 accctggcaaaaggaacttcgcggtggtagaagctggcgcgatcgatccacaaag 176
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Db 556 ACAATCGCAAGGCGAATTTTCAAAAGTAATTTGGCAAGACATATCTTACAGGCA 615
QY 177 caggttcgaataaataatgatataaacaagatagatcaagaatttggaaatc 236
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Db 616 GAGGTTGCAATTAATAATTTGACAAACTGTTGAATCCAAAGTCTACAAAAAGCTC 675
QY 237 taccgtgagttcagctgatgaagcttcgaaacctccacacatataaagttaccg 296
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Db 676 TTCAGAGAACTAGATATATGAGATTTTAATCATCCAAATATGATGATTTATTCGA 735
QY 297 gttatgaaacaagaagacatgctttacatcgcactgaattgtcaaaataggaaatg 356
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Db 736 GTCATTTGAACAGAAAAAACACTACTAATCATGATGATATGCAAGTGCAGTGAAGTA 795
QY 357 ttgatatttgacttccaacggcaccctgagtagaagcagcgcggaagaagttctg 416
   || || || || || || || || || || || || || || || || || || || || ||
Db 796 TTTGACTATTTGGTTGCACATGCGAGATGAAGAAAAAGAACGATCTAAATTTAGA 855
QY 417 caaatccgtcggccgtggagtagtgcagaccatcacatcgatcccggaacctcaag 476
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Db 856 CAGATTGCTGCTGCAGTTCAATACTGCAATCGAAGAACGAGATGTCATCGAAGACCTCAG 915
QY 477 accgaaacctcctcgtgtagtgcacacatgacatcaagctgcagatttggattgg 536
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Db 916 GCTGAAATCTATTTGTATGATGCCGATATGAACATTTAAATGCGAGATTTGGTTTAC 975
QY 537 aattctcaagtcaggaagacctctgccacgtggtgtggagcccccgatccgccc 596
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Db 976 AATGAATTTACTGTTGGCGGTAACTCGACACGTTTGTGGCAGTCTCCATTAACGCA 1035
QY 597 ccggaagctcttgaagggaagagatagaagcccccgatgacatctggagccctggc 656
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Db 1036 CCGTAGCTCTTCAGAGCGCAAGAAATATACGGCCAGAAAGTGGATGTGTGGATCGGG 1095
QY 657 gtggtcgtacgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 716
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Db 1096 GTCAATTTATACACACTGAGTCAAGTGTGCTACCTTCCCTTGAATGGGCAAACTTAAGGAA 1155
QY 717 ctgagacagcggtgctgtagaagcgccgtccgcacatccctctcatgtctcaagctgt 776
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Db 1156 CTGAGAGGAGAGATTTAAGAGGAAATACAAATTTCCCTTCTACATGCTTACACACTGT 1215
QY 777 gagaagcctgcacccgcagatgctgtgtgtgtagaccccgcaagcgcatcacatcgccag 836
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Db 1216 GAAAACTTCTCAAAAGTTTCTGCTGCTAATCAATTTAAACGCGGCACTTACAGCA 1275
QY 837 atccggcagcagcggtgtagtgcgggtgagc 867
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Db 1276 ATCATGAAGGACAGGTGATCATATGCAGGCG 1306

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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA of rat
; OTHER INFORMATION: Liver AMP protein kinase
US-08-557-006C-24

Query Match      8.0%; Score 203.2; DB 4; Length 2761;
Best Local Similarity 53.9%; Pred. No. 1.2e-34;
Matches 440; Conservative 0; Mismatches 373; Indels 3; Gaps 1;

QY 44 cagcgcgagcccgcgccgagcgaagatgaagccagcagaagccccctcggtgtgtttaa 103
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Db 11 ccgcgcgccgaacatggtcgaagaagcagaagcagcggtgtgtgaagatcgaacacta 70
QY 104 cgacatcgagcgagccctgtgcaaaagcacttcgcgtgtgtgaagctggcgcgatcg 163
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Db 71 cgtgctggggagacaccttggcgctgcgcaccttcggcaagtgaaatggaagacataca 130
QY 164 agtcccaaaacgcaggtgtgcaataaaataatgataaaacagat--agattcaag 220
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Db 131 attgcaagccataaagtgagcagttgaatgatttaaaatagacagaagattcgagttaga 190
QY 221 caatttggagaataatctacgtgtaggttcagctgtgaagctcttgaacctcacat 280
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Db 191 tgttgtgaaaaataaaacgagaatltcaaaatccttaaccttctgcatactcatat 250
QY 281 cataaagcttaccaggttatgaaacaaagacatgctttacatcgtacatgaaatttcg 340
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Db 251 tatcaacctctacaaagtatcatgacatcccaacagacttttattggtatggaatgt 310
QY 341 taaaaatggagaagaatgtttgatatttgacttccaacgggcaccttgatgagaacgagcg 400
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Db 191 tgttgtgaaaaataaaacgagaatltcaaaatccttaaccttctgcatactcatat 250
QY 281 cataaagcttaccaggttatgaaacaaagacatgctttacatcgtacatgaaatttcg 340
   || || || || || || || || || || || || || || || || || || || || ||
Db 251 tatcaacctctacaaagtatcatgacatcccaacagacttttattggtatggaatgt 310
QY 311 gctctgaggtgtagttgttcgactacatctgtaaacacgagaggtgtgaagaggttgaagc 370
   || || || || || || || || || || || || || || || || || || || || ||
Db 401 gggagaagatgtctgcaaatcctgttcgacgtgtgagtagtcttccagacatcacatcgt 460
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Db 371 tgcgagctctccagcagatcttgcgtcgtgcgtgactctgttccaaagacatgtgt 430
QY 461 ccacgggaccccaagacccgaacacccctcgtctgtgtagtgaacatgacatcaagctgcg 520
   || || || || || || || || || || || || || || || || || || || || ||
Db 431 ccacgggacccgaagccagagacgtgtgtctgtgtagcgcagatgagatgacgaatagc 490
QY 521 agatttggatttgggaatttctacaagtcaggaagcctctgtccagctgtgtgtggag 580
   || || || || || || || || || || || || || || || || || || || || ||
Db 491 tgacttcgagactctctaatatgtatgtcagatgtgaatttctacgaactagctgtgagtc 550
QY 581 ccccccttatgcccccggaagcttcttgaagggaaggaattgaagggccccacgtgga 640
   || || || || || || || || || || || || || || || || || || || || ||
Db 551 gccaaattatgacagcaggaaggtcatctcaagaaagcgtcatgctgggtcccgaggttga 610
QY 641 catctgagacccctggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 700
   || || || || || || || || || || || || || || || || || || || || ||
Db 611 tatctgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 670
QY 701 gcttaacctgcagcgtgtgagacagcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 760
   || || || || || || || || || || || || || || || || || || || || ||
Db 671 tgagcagctgtcctacgctctttaaagaagatccgaggggtgtgtgtgtgtgtgtgtgt 730
QY 761 catgtctaaagctgtgtgagagccttatccgcgacgtgtgtgtgtgtgtgtgtgtgtgt 820
   || || || || || || || || || || || || || || || || || || || || ||
Db 731 tctcaaccttctatctgcacactgtgtgatgaacatgtcgaagctgtgaaccttgaagcg 790
QY 821 catcacatcgccagatcgccagacacacggtgagat 856
   || || || || || || || || || || || || || || || || || || || || ||
Db 791 agcaactatcaaaagacatacagagagcatgaaggtc 826

```

RESULT 3


```

Db 310 gctgcactacatctgttaaacacgagaggttgaagaagtgtgaagctcgcgcgtcttcca 369
Qy 416 gcaaatctctgcgcgttggagtaactgtacagacatcatcgtccaccgagacctcaa 475
Db 370 gcaagattctgtcgtcgtgactactgtcacagacatggtgttccacagagacctgaa 429
Qy 476 gaccgagaacccctcgtcgtgagtaacagatgacatcaagctggagatttggatttgg 535
Db 430 gccagagaacggtgttgcgtgacgcccagatgaatgaatgaatgaatgaatgaatgaat 489
Qy 536 gaatttctcaagatcagagagagcctctgtccacgtgtgtgtgtgtgtgtgtgtgtgtgt 595
Db 490 taatatgtatgtaagatgtgtgaattcttaagaactagctgtgtgtgtgtgtgtgtgtgt 549
Qy 556 cccggaagcttcttgagggaagatgaagagcccccagctgtgacatcttgagctgg 655
Db 550 accgagagtcacatcagagaagagctgtatgtcgtgtgtgtgtgtgtgtgtgtgtgtgt 609
Qy 656 cgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 715
Db 610 tgtatccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 669
Qy 716 gcttgagacagcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 775
Db 670 gctcttgaagaagatcccgaggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 729
Qy 776 tgaagaccgtgacccgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 835
Db 730 tgcacctcgtgtagatgcatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 789
Qy 836 gatccgagcagccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 856
Db 790 catagagagcatgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 810

```

RESULT 5

US-09-101-146-44
Sequence 44, Application US/09101146
Patent No. 6124125

GENERAL INFORMATION:

APPLICANT: Dartmouth College, St. Vincents Institute of
APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101.146
FILING DATE: October 7, 1998

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:

LENGTH: 1647

```

; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-101-146-44

```

Query Match 7.6%; Score 192.6; DB 3; Length 1647;
Best Local Similarity 54.2%; Pred. No. 1.8e-32;
Matches 434; Conservative 0; Mismatches 364; Indels 3; Gaps 2;

```

Qy 59 gggcagagctcagggccagacagaagcccccctgggtgtgtgtgtgtgtgtgtgtgtgtgtgt 118
Db 3 gggcagagctcagggccagacagaagcccccctgggtgtgtgtgtgtgtgtgtgtgtgtgtgt 62
Qy 119 ccttgagcaaaagcaacttcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 178
Db 63 GCTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGTGGGCGT 122
Qy 179 gttgcaataaataatgata-aaacagattagatccaagcaatt--tggagaataat 235
Db 123 AGTTGCTGTGAAGATTAATCAACCGCAGAGATTCGAACCTTGACGTGTGTGTGTGTGTGTGT 182
Qy 236 ctatcgtgagctcagctgtatgaagctcttcgaacacatccacatcaataaagctttac 295
Db 183 CCGCAGAGAGATCCAGAACCTGAGCTTTTCAGGCGACCTCATATATATCAACTGATACCA 242
Qy 296 gattatgaacaacaagagatgcttcttaccatgcctgaatgtgtgtgtgtgtgtgtgtgtgt 355
Db 243 GGTTCATCACTACACCGTCTGATATTTTCATGCTCATGATGATATGCTCATGAGAGAGCT 302
Qy 356 gtttgaattatgaacttccacagagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 415
Db 303 ATTGATTTATCTGTAAATGAAGTGTGACGAAATGAAGAGTGCAGCTGTGTGTGTGTGTGTGT 362
Qy 416 gcaaatctctgcgcgttggagtaactgtacagacatcatcgtccaccgagacctcaa 475
Db 363 GCAGATCCTTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
Qy 476 gaccgagaacccctcgtcgtgagtaacagatgacatcaagctggagatttggatttgg 535
Db 423 ACCTGAAACGTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
Qy 536 gaatttctcaagatcagagagcctctgtccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
Db 483 AAACATGATGTGATGATGTGATTTTAAAGACGACCTGTGCTGCCCAATATATCTGTC 542
Qy 596 cccggaagcttcttgagggaagatgaagagcccccagctgtgacatcttgagacttgg 655
Db 543 ACCAGAGATTAATTCAGGAAGATTCACGACGACCTGGAAGATGACATCTGGACGCGG 602
Qy 656 cgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 715
Db 603 GGTCAATCTCTATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 662
Qy 716 gctgaagacagcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 775
Db 663 TCTTTTAAAGATGATGATGATGATTTTAAATACCCCTCAATATTAATCCCTCTGT 722
Qy 776 tgaagaccgtgacccgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 835
Db 723 AATTAACCTTTGAACCATATGCTGACGAGTAGATCTTATGAMAGGGCCACATTAAGAA 782
Qy 836 gatccgagcagccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 856
Db 783 TATCAGGAAACATGATGATT 803

```

RESULT 6

US-08-557-006C-44
Sequence 44, Application US/08557006C
Patent No. 6258547

GENERAL INFORMATION:


```

; APPLICANT: Berl, Rajindar K.
; APPLICANT: Carling, David A.
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NCAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-44
```

```

Query Match          7.0%; Score 177.6; DB 4; Length 1747;
Best Local Similarity 53.8%; Pred. No. 36-29;
Matches 434; Conservative 0; Mismatches 364; Indels 8; Gaps 3;
```

```

Qy 59 gggcagagtcaggcgccagagagccctccggtggtgtttaaagacacgcgac 118
   || || || || || || || || || || || || || || || || || || ||
Db 3 ggcctgagagcagagacagacagcggtgtgaaagtcgcacactacgtgtcgagac 62

Qy 119 cctgggcaagagcaacttcgcggtgtgtgaagtcggtcggtgacatgcacaaacgca 178
   || || || || || || || || || || || || || || || || || || ||
Db 63 cctgggctgcgcaccttcgcgcaagtgaaagattggaacacaaatgcagcgcaaa 122

Qy 179 ggttgcaataaataattgatataaacagatt---agattcaagcaatttgagaanaat 235
   || || || || || || || || || || || || || || || || || || ||
Db 123 agtggcaglttaagattctaataatagacagaagattcgcaggttttagatgtgtggaanaat 182

Qy 236 ctatctgagagttcagctgtagagcttctgaaacatccacacataaagctttaacca 295
   || || || || || || || || || || || || || || || || || || ||
Db 183 aaaaacgagaatccaataatctaactcttctgcaatccctcatatatacacaatccacaa 242

Qy 296 ggttatggaacaaagacatgcttaccatcgtcactgaatttgcctaanaaavgagaat 355
   || || || || || || || || || || || || || || || || || || ||
Db 243 agtgaatcagacactccacacagacttttattgttaattgaaatattgtcttgaggtgaatt 302

Qy 356 gtttgatttttgacttccaaacgggcaacctgagtgaagcagagcgcggaagaattcttg 415
   || || || || || || || || || || || || || || || || || || ||
Db 303 gtttcgactacatctgtaaacacgggaggttgaaaggtggaagctccgcggtcttcca 362

Qy 416 gaaaatcctctcgccggttgagtaactg---tcaagaccatcacatctccacgggacctc 473
   || || || || || || || || || || || || || || || || || || ||
Db 363 gcaagattcgtctgcgcgtgagactactgctcacaagcaactgtgtctccacagggacctg 422

Qy 474 aagacgggaacactcctgctgtgagtgcacaatgagacatcaagctgtgcagatttgattc 533
   || || || || || || || || || || || || || || || || || || ||
Db 423 aagcgggaagaaactgtgtgtgagcggccagatgaatgactaagaatactgtgacttcgaaatc 482

Qy 534 gggaaattctcaagagtcagagagagcctctgtccacgtgtgtgtgagggcccccgtatgcc 593
   || || || || || || || || || || || || || || || || || || ||
Db 483 tctaaatagatgtcagatgtgtgaattcttaagaaactagctgtgtgacgcgaatattatgca 542

Qy 594 gcccgcgaagactcttgagggaagagtaatgaagcccccagcttgagacatctgagacctg 653
   || || || || || || || || || || || || || || || || || || ||
Db 543 gcaaccggaggtcatctcaggaagagctgatacggtctccctgaggttgatatctgagagctgt 602

Qy 654 ggcgtgtgtctgtgaagctctgtgtctgtctcccttcctcccttcgatagtggcct---aaactgt 710
```

```

Db 603 ggtgtatcccgtagtcgcttctctctgtgcaacctccctcggtgcagacgatgacagctg 662
Qy 711 ccgagctgagagacagcggtgtgtgaggcgccgtccgcacatccctcttcaatgtctcaa 770
   || || || || || || || || || || || || || || || || || || ||
Db 663 cctaagctttaaagaagatccgaggggtgtgttctcaatcccgaggtatctcaaacgt 722

Qy 771 gactgtgagagcctgtatccgcgcagatgctgtgtgtgaaccccgccagcgcatcacatc 830
   || || || || || || || || || || || || || || || || || || ||
Db 723 tctattccactctgtcgtatgacatgtcgaggttgagcccttgaaagcgagcaactatc 782

Qy 831 gcccaattccggcgccagcccggtgat 856
Db 783 aagacatacagagagcatgaattgtt 808
```

RESULT 7

```

US-08-557-006C-37
; Sequence 37, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Berl, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NCAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat liver AMP
; OTHER INFORMATION: protein kinase
US-08-557-006C-37
```

```

Query Match          7.0%; Score 177; DB 4; Length 1736;
Best Local Similarity 52.2%; Pred. No. 41e-29;
Matches 418; Conservative 0; Mismatches 380; Indels 3; Gaps 1;
```

```

Qy 59 gggcagagtcaggcgccagagagccctccggtggtgtttaaagacacgcgac 118
   || || || || || || || || || || || || || || || || || || ||
Db 3 ggcctgagagcagagacagacagcggtgtgaaagtcgcacactacgtgtcgagac 62

Qy 119 cctgggcaagagcaacttcgcggtgtgtgaagtcggtcggtgacatgcacaaacgca 178
   || || || || || || || || || || || || || || || || || || ||
Db 63 gctgggctgcgcaccttcgcgcaagtgaaagattggaacacataatcaacagcgcaaa 122

Qy 179 gtttgatttttgacttccaaacgggcaacctgagtgaagcagagcggtgagaaattcttg 235
   || || || || || || || || || || || || || || || || || || ||
Db 123 agtggcaglttaagattctaataatagacagaagattcgcaggttttagatgtgttgaanaat 182

Qy 236 ctatctgagagttcagctgtagagcttctgaaacatccacacataaagctttaacca 295
   || || || || || || || || || || || || || || || || || || ||
Db 183 aaaaacgagaatccaataatctaactcttctgcaatccctcatatatacacaatccacaa 242

Qy 296 ggttatggaacaaagacatgcttaccatcgtcactgaatttgcctaanaaavgagaat 355
   || || || || || || || || || || || || || || || || || || ||
Db 243 agtgaatcagacactccacacagacttttattgttaattgaaatattgtcttgaggtgaatt 302

Qy 356 gtttgatttttgacttccaaacgggcaacctgagtgaagcagagcgcggaagaattcttg 415
   || || || || || || || || || || || || || || || || || || ||
Db 303 attgactacatctgtgaagcagaggttgaaagatatgaaagcagcggtccttcca 362
```

```

QY 416 gcaatcctctgcgcgctggaagtactgtcacgaccatcacatcgtccacgagccttaa 475
D 363 gcaatctctgtctgtctgtgacttactgtcatagacatagtgttcttcacgagaccgtaa 422
QY 476 gaccgaagacctcctcgtcgtggaagcaacatggaacatcaagctgcgaagtattggaattgg 535
D 423 accgagagatgtcctctgtgtgacacacatgaaatgcacaaagaaagacgatttcgattatc 482
QY 536 gaattctacaagtcaggaagacctctgtccacgtgtgtgtgagagcccccgtatgcgcg 595
D 483 taatgatgtcagatgtgtgaattctcgtagaactagtttgcgacatcccaattatgcagc 542
QY 596 ccggaagctcttgaagaggaagagatgaagcccccacgtgacatctggaagcctggg 655
D 543 accggaagatctcgaagcagatgtatgacaggtccctgaagattgatactcggagctgtgg 602
QY 656 cgtgtgtcgtacgtctcgtctcgtgtctctccctctgattgagagcctaactgcgcgac 715
D 603 tgtatctgtatgtcctctctcttctgtggcacccctcccaattgaaatgagcatgtacctac 662
QY 716 gctgagacagcggtgtctgtagagcgccgtctccgcatccctctcattgctcaagactg 775
D 663 gttatttaagaagatccgaagggtgtctttattatcccaaatatcattcattcgttctgt 722
QY 776 tgaagacctgacccgcgcgcatgtgtgtgtgagcccccgcgaagcgatcaacatcgccca 835
D 723 cgcactctcctgtatgcatactgtcgaaggtgacccactgaaacgagcaactatacaaga 782
QY 836 gatccgcgacgacccggtgat 856
D 783 cataagagagcatgaatggt 803

```

RESULT 8
 US-08-557-006C-36
 ; Sequence 36 Application US/08557006C
 ; Patent No. 6258347
 ; GENERAL INFORMATION:
 ; APPLICANT: Berl, Rajinder K.
 ; APPLICANT: Carling, David
 ; APPLICANT: Forde, Robert A.
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
 ; FILE REFERENCE: NCAP/PHM37588/OST
 ; CURRENT APPLICATION NUMBER: US/08/557.006C
 ; PRIOR FILING DATE: 1996-03-06
 ; PRIOR APPLICATION NUMBER: PCT/GB94/01093
 ; PRIOR FILING DATE: 1994-05-20
 ; PRIOR APPLICATION NUMBER: GB 9310489.1
 ; PRIOR FILING DATE: 1993-05-21
 ; PRIOR APPLICATION NUMBER: GB 9318010.7
 ; PRIOR FILING DATE: 1993-08-31
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 36
 ; LENGTH: 1783
 ; TYPE: DNA
 ; ORGANISM: Human AMP protein kinase
 ; US-08-557-006C-36

Query Match 7.0%; Score 177; DB 4; Length 1783;
 Best Local Similarity 52.2%; Pred. No. 4.1e-29;
 Matches 418; Conservative 0; Mismatches 380; Indels 3; Gaps 1;

```

QY 59 gggccagagtcagagcagagagagcccccctcgggtgtgttttaacacatcgagcgagac 118
D 4 ggtctgagagcagagacagacagcggtgtgaaagatcgcagacatcagtcgtgtggcgacac 63
QY 119 ccttgagcaagcgaactctgcgtgtgtgaaagctgtgcgcgagctcggttaccacaacgca 178
D 64 gctgggcgtcgcgaccttcggaacagtgaaattggaacatcaatcaacagcgccataa 123

```

```

QY 179 ggttgcataaataatgtata--aaacacgattagattcaagcaatttgagaataat 235
D 124 agtgcagtttaaatcttaataatgacaggaagatcgcgaatttgatgtctgtgaaataat 183
QY 236 ctatcgtgaggttcaactgtatgaagctcttgaacacatccacatcaataaagcttacc 295
D 184 aaaaaggaagatccaataatcaaacctctctgtcattccatcattatcaaacataacca 243
QY 296 ggtatgaaacaaagagacatgctttacatcgtcactgatttgcctcaaaaatvgagaat 355
D 244 ggtgatcagacccccaacagatcttlttatgtgaaatggaatagtgtctggaagtgaaat 303
QY 356 gtttgattattgaattccaaacgggacactgaaatgaaacgagcgcggaagaagtctg 415
D 304 attgtacatcatctgaaacatgagcgggttgaagagatggaagccagcgctcttca 363
QY 416 gcaaacctcgtcgcgctgagatgactgtacgacacatccatcgcgtccacggagactcaa 475
D 364 gcaatctcgtcgtcgtgtgtatgaatcgtcatatgacatagtgttcatcagagactgaa 423
QY 476 gaccgagaacctcctcgtgtgaaacacatggaacatcaagctgcgagatttgattgg 535
D 424 accagagaatgtccctgtgtgtgtgacacacatgaaatgaaagacgacttgcgattac 483
QY 536 gaattctacaagtcaggaagacctctgtccacgtgtgtgtggaagcccccgtatgcgcg 595
D 484 taatgtatgtatgaatgtgtgaattcttgaagaactagttgcgacttccaaattatgcagc 543
QY 596 ccggaagctcttgaaggaagagatgaagagcccccagcgtgagacatctgagcctgg 655
D 544 accatgaagcatcctcagcgagatgtatgacaggtgtcctgaagtatgatactcgtgagc 603
QY 656 cgtgtgtgtgaagctcgtcgtgtgtcctcctccctcgtatgagcctaaacctgcgcgac 715
D 604 tgtatctgtatgtcctctctgtgtgtgacccctcccatlttatgtatgacatgtacctac 663
QY 716 gctgagacagcggtgtcgtgagagcgctctccgcatccctctcattgttctcaagactg 775
D 664 gttatttaagaagatccgaagggtgtgtctttattatcccaaatatcattcattcgtt 723
QY 776 tgaagacctgacccgcgcgcatgtgtgtgtgagcccccgcgaagcgatcaacatcgccca 835
D 724 cgcactctcctgtatgatalatgtcgcaggttgaccacatgaacgagcaactatcaaga 783
QY 836 gatccgcgacgacccggtgat 856
D 784 cataagagagcatgaatggt 804

```

RESULT 9
 US-09-212-771-1
 ; Sequence 1 Application US/09212771
 ; Patent No. 5958773
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
 ; FILE REFERENCE: RTS-0034
 ; CURRENT APPLICATION NUMBER: US/09/212,771
 ; CURRENT FILING DATE: 1998-12-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 1
 ; LENGTH: 2610
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (199)..(1641)
 ; US-09-212-771-1

Query Match 4.0%; Score 102; DB 2; Length 2610;
 Best Local Similarity 50.6%; Pred. No. 5.5e-13;

```
Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 120 ctgggcaaaagcaactcgcgtggtgaaagctggcgcgacatcagatcaccacaaacgag 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 ctgggcaaaagcaactcgcgtggtgaaagctggcgcgacatcagatcaccacaaacgag 723
QY 180 gtgcgaataaataatgatataaacgattagattcaa---gcaattggagaanaatc 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 taagccatgaagatcctcagaagaagatcatcgtggcgaagcgaggtgccccacaca 783
QY 237 taatcgtgaagttcagatgaagaactctgaacacatccacacatcaaaactttacag 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 784 ctacacggaacccgcgtctcgaagaactccagacaccccttcacacgcccctgaagtac 843
QY 297 gtatggaacaaagacatgtcttacatcgtcactgaattgtctaaatgaggaatg 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 844 tcttcacagccacgacgacctgtctgtctgtaagtagtaagcacaacgggggagagctg 903
QY 357 ttgcattatctgaacttccaaacgggacactgaatgaagaagcgcgaggaagattctg 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 904 tcttcacacgtctccgggaacgtgtgtctccgaagacggcgccgtctctatgagct 963
QY 417 caaatccgtcgcgcgtggaggtactgtcac---gacatcaacatcgtccacgggaactc 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 964 gaagattgttcaagcccttggaactcgtcactcgtgaagaagacgtgtgtacccgggaactc 1023
QY 474 aagacggaacactcctcgtcgtatggaacatgacatcaacgtcgcagatttgattt 533
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Db 1024 aagctggaagaactcatgctggaacgaagacggaacttaagatcaacagacttgggctg 1083
QY 534 gggaaattctca---caagtaagaagagcctctgtcacaagtgtgtggagcccccgat 590
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Db 1084 tgcagaaggaaggatcaagagcggtgtccacatgaagaactcttgcgcacccctgaagtac 1143
QY 591 gccgcgccgggaagctcttggagggaaggaagatgaaggccccccacggcggaacttgagc 650
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Db 1144 ctggcccccgaggtgctggaggaacatgaactac---ggcggtcagtggaactgtgagggg 1200
QY 651 ctgggctggtgctgtacgtcgtctgtcgtctcctccctcgtatggtggaactcgtg 710
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Db 1201 ctgggctggtgtacgtatgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 711 ccgaagctggaacagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 770
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Db 1261 gaagaagcttcttgagctcatcctcatgtgaagagatccgcttccgcgcagcgtgtgtccc 1320
QY 771 gactgtgagagcctgatccgcgcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 812
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RESULT 10
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmlings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091, 058
; EARLIER FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: CDS
LOCATION: (199)..(1641)
US-09-091-058-1
Query Match 4.08; Score 102; DB 3; Length 2610;
Best Local Similarity 50.68; Pred. No. 5.5e-13;
Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 120 ctgggcaaaagcaactcgcgtggtgaaagctggcgcgacatcagatcaccacaaacgag 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 ctgggcaaaagcaactcgcgtggtgaaagctggcgcgacatcagatcaccacaaacgag 723
QY 180 gtgcgaataaataatgatataaacgattagattcaa---gcaattggagaanaatc 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 taagccatgaagatcctcagaagaagatcatcgtggcgaagcgaggtgccccacaca 783
QY 237 taatcgtgaagttcagatgaagaactctgaacacatccacacatcaaaactttacag 296
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Db 844 tcttcacagccacgacgacctgtctgtctgtaagtagtaagcacaacgggggagagctg 903
QY 357 ttgcattatctgaacttccaaacgggacactgaatgaagaagcgcgaggaagattctg 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 904 tcttcacacgtctccgggaacgtgtgtctccgaagacggcgccgtctctatgagct 963
QY 417 caaatccgtcgcgcgtggaggtactgtcac---gacatcaacatcgtccacgggaactc 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 964 gaagattgttcaagcccttggaactcgtcactcgtgaagaagacgtgtgtacccgggaactc 1023
QY 474 aagacggaacactcctcgtcgtatggaacatgacatcaacgtcgcagatttgattt 533
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1024 aagctggaagaactcatgctggaacgaagacggaacttaagatcaacagacttgggctg 1083
QY 534 gggaaattctca---caagtaagaagagcctctgtcacaagtgtgtggagcccccgat 590
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Db 1084 tgcagaaggaaggatcaagagcggtgtccacatgaagaactcttgcgcacccctgaagtac 1143
QY 591 gccgcgccgggaagctcttggagggaaggaagatgaaggccccccacgtggaactcgtg 650
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1144 ctggcccccgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
QY 651 ctgggctggtgctgtacgtcgtctgtcgtctcctccctcgtatggtggaactcgtg 710
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Db 1201 ctgggctggtgtacgtatgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 711 ccgaagctggaacagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 770
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1261 gaagaagcttcttgagctcatcctcatgtgaagagatccgcttccgcgcagcgtgtgtccc 1320
QY 771 gactgtgagagcctgatccgcgcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 812
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Db 1321 gaggcgaagctcctgtcttcaagggtgtgtcacaagaagacccc 1362

RESULT 11
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RPS-0035
; CURRENT APPLICATION NUMBER: US/09/256, 465
; EARLIER FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
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```
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0465 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1929 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MMLR1DT01
CLONE: 472480
US-09-016-000-10
```

```
Query Match          3.8%; Score 96.6; DB 2; Length 1929;
Best Local Similarity 51.3%; Pred. No. 7.1e-12;
Matches 250; Conservative 0; Mismatches 234; Indels 3; Gaps 1;
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Oy 60 ggcacagatcagcgccagcagagcccccctcgggtgtttttacagacatcgagcgc 119
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Db 320 gccacacctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 379
Oy 120 ctgggcaagagcaacttcgcggtgtgtaagctggcgcgatcgagtcaccacacgcag 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 cttggcggaagcgtctttttccacggtgtctgcgcgcgcgcgcgcgcgcgcgcgc 439
Oy 180 gtggcaataaaatattgataaacac---gattgattcaagcaatttggagaatac 236
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Db 440 taagcatttaaaattctggagacgcacatattatataaagacagctccctattgta 499
Oy 237 tatcgtgaggttcagctgtatgaagcttctgaaccatcacacatcataaagctttacag 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 accagagaggggatgacatgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 559
Oy 297 gttatggaagaaagagacatgctttacatcgtcaactgaaatttgcataaagtgaaatg 356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 560 acatttcagagacacgacgagcgtatttgcgccttattgacaaataatggagacta 619
Oy 357 ttgatatttgacttcccaacgagcaccgtgagtgagaagcagcggaagaattctg 416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 620 ctttaattatttgcgcaaaatcgcttcttcatgtgacagacgttaccctttttacacgct 679
Oy 417 caaatcctgtcgcgcgtgagtgactgtcagacacatcacatcgtccacgcggagctcaag 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 gagattgtctctcttttagagtaatttcacagcgacgacatcattcacagggactttaa 739
Oy 477 accgagaacctcctgtgtgagtgcaacatgagacatcaagctgagatttggattggg 536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 740 ccggaaaacattttgttaattgaagatgacacatccagatccagattttggaaacagca 799
Oy 537 aatttct 543
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Db 800 aaagtct 806
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RESULT 14
US-09-289-466-2
Sequence 2, Application US/09289466A
Patent No. 6124272
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION
FILE REFERENCE: RTS-0060
CURRENT APPLICATION NUMBER: US/09/289,466A
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CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 2
LENGTH: 1890
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (80)..(1750)
US-09-289-466-2
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Query Match          3.8%; Score 95; DB 3; Length 1890;
Best Local Similarity 51.1%; Pred. No. 1.6e-11;
Matches 249; Conservative 0; Mismatches 235; Indels 3; Gaps 1;
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Oy 60 ggcacagatcagcgccagcagagcccccctcgggtgtttttacagacatcgagcgc 119
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Oy 120 ctgggcaagagcaacttcgcggtgtgtaagctggcgcgatcgagtcaccacacgcag 179
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Db 341 ctggggaagcctcttttccacggttctgtcgtcgagacatgcaacctccagagaa 400
Oy 180 gtgcaataaaatattgataaacac---gattgattcaagcaatttggagaatac 236
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Db 401 tatgattaaattcttggagaagcgcacatataaaagagaagaagttccctatgta 460
Oy 237 tatgtaggttcgcgtgtatgaagcttctgaaccatcacacatcataaagctttacag 296
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Db 461 accagagagcggtatgtatgtcgtcgtgacacccctcttgttaagctttactc 520
Oy 297 gttatggaagaaagagacatgctttacatcgtcaactgaaatttgcataaagtgaaatg 356
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Db 521 acatttcagagcagaaagaaactgatttgcgccttattatgccaanaatggagaacta 580
Oy 357 ttgatatttgacttcccaacgagcaccgtgagtgagaagcagcggaagaattctg 416
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Db 701 ccggaaaacatttgttaattgaagatagatgcacatccagatccagatttggaaacagca 760
Oy 537 aatttct 543
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Db 761 aaagtct 767
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RESULT 15
US-09-467-082-3
Sequence 3, Application US/09467082
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESI
CURRENT APPLICATION NUMBER: US/09/467,082
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 2549
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (81)..(1136)
NAME/KEY: unsure
LOCATION: 6
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OTHER INFORMATION: unknown
US-09-467-082-3

Query Match 3.5%; Score 88.4; DB 4; Length 2549;
Best Local Similarity 47.5%; Pred. No. 4.5e-10;
Matches 365; Conservative 0; Mismatches 391; Indels 12; Gaps 3;

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Db 186 cagaacacagccacttgatcagtttgaacgaatcaagaccctcgacggctcttc 245
QY 138 gcggtgtggaagcttgcgctgcatcgatcaccacaacgcaagtttgcataaataat 197
Db 246 gggcggtgtgagctgtgtgaacaagaagacgggaaccactatgccatgaagatcc 305
QY 198 gataaacaagattag---attcaagcaatttggagaataatcgtgaagttcagctg 254
Db 306 gacaacaagaagtggtgtgaactgaacagatcgaaacacaccctgaatgaagaagcgatc 365
QY 255 atgaagctctgaaccatcacacataaaagctttacaggttatgtgaacaagaagac 314
Db 366 ctgcgaagctgaacttcgcttcgttccgtcaaacctcgatctcctcaaggacactca 425
QY 315 atgctttacatcgtaactgaatttgcataaataatgagaagaattgttatattgactcc 374
Db 426 aactatacatgtcatgtgaagtaacgtgcgcgaggaatgttctcacacctacgcgcg 485
QY 375 aacgggcaaccctgaatgaagaagcgagcggaagaagttctgcaaatcctgtgcgcgtg 434
Db 486 atcggaaggttcagtgagcccatgcccgtttctacgcgcgcacagatcgtcctgaacttc 545
QY 435 gagtactgtcagacatcacatcgttcacacggagacctcaagaaccgaaacctcctgtg 494
Db 546 gagaatctgcactgctgtgcatctcatcacagagacctgaagccgagaaatcgtcatt 605
QY 495 gatggcaaatggaatcaatcaagcttgagatttggatttggaaattctacaagtcagga 554
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Search completed: March 22, 2002, 13:20:03
Job time: 8941 sec

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RESULT	3		
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LOCUS			
DEFINITION	BF783804	924 bp	EST
	60210972AF1 NC_1	CGAP_K1d14 Mus musculus	CDNA clone IMAGE:4238068
	5', mRNA sequence.		
ACCESSION	BF783804		
VERSION	BF783804.1	GI:12088640	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
	1 (bases 1 to 924)		
REFERENCE	NIH-MGC	http://mgc.ncl.nih.gov/	
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT			

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLAM848 row: p column: 05
 High quality sequence stop: 681.
 Location/Qualifiers

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FEATURES
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      /organism="Mus musculus"
      /strain="FVB/N"
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      /clone_1="IMAGE:4238068"
      /clone_1b="NCI_CGAP_Kid14"
      /lab_host="DH10B (71 phage-resistant)"
      /note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
      Average insert size 1.75 kb. Constructed by Life
      Technologies. Note: this is a NCI_CGAP library. |"
BASE COUNT
  214 a 322 c 246 g 142 t
ORIGIN

```

Query Match	13.18	Score 344.8	DB 11	Length 924
Best Local Similarity	73.48	Pred. No. 1.3e-38		
Matches 511	Conservative	0	Mismatches 172	Indels 13
			Gaps	
Qy	882	ctgatccgcgcgaatgcgcgtggtgtgtggaacccgcagagcgcatatccatctgcccagatccgg	941	
Db	2	CTGATCAGACGCATGCTGGTGTGGAGCCCGCTAAACGGATCAACCTAACCCAGATCCGC	61	
Qy	942	cagacccgtgtgagtgcgtgagcttgagccctgtcttgcggagaccgcctcgcgcctctcc	1001	
Db	62	CAGACCCGGTGGATGACGAGGCCGACCCCACTCTCTCTCAGCAGAGATGACCTTCCTTGAC	121	
Qy	1002	gcacacagctacacactccaaaccttgcgcagactacgatagagcagcgctgtgatactatgcag	1061	
Db	122	ATGCAGAGCTACACCTCCACCTGTGGGGAGATTAAAGAAAGAGTGTAGGATTCATGGAG	181	
Qy	1062	acccttggcgttggaccgcggcagagagcgcttggatcaacttcaaaacagcagctataccac	1121	
Db	182	GCCTTCGGCATTCGACCGCGAGCGAGCTATAGATCTCTCAGACAGCAGCTACAACAC	241	
Qy	1122	tttgcgtcaattatatacccccctcttggcgcgtctaaagatgatatcggaattgccag---	1178	
Db	242	TTTCCGCGCATTAATCACTCTCTACTGAGCGGCTTAAGAGAGATGAAGCGCGCCAGCC	301	

Qy	1179	----	tgagcccccgcgcggccgctgcagagcagccgcgctctgagctcgcagctcagtg	1234
Db	302	TCATCCGGCCACACCTTACCCACAGACAGGCCAGCTCCGAAGCTCAGACTCAGAG	361	
Qy	1235	cttggaagctgcctcaggaagbctttccacgcgaccctttccgactgcct-tgctgtgc	1293	
Db	362	TCTGGAGTTCCTCTCAAGAAATTTCTCCCGTGAGACCTTCCGGCCCTCTGTGCTGTC	421	
Qy	1294	cgcagccgcagacacttgctgcagctcctccacagccgcgagatgagcgtgtagctccaga	1353	
Db	422	CACAGCCCCAGGCCCTGGCTCAGTCTGTCTTCAGAGGCTGAATATACGTATCTCCACA	481	
Qy	1354	gctgcgtcagtgagcccttgctcttcccgaggatgacagcttgacgagtggtcttcggc	1413	
Db	482	GCTCACTTCA--GECCTTATATTATTCCTCCCTGGATACACTGTGAGTGTCCGG-	537	
Qy	1414	ccggcccgctgtccccaagcagcgcctgcctgcagca-cagcatcagtgaggaagccagagag	1472	
Db	538	CACGATTCATCTCCCCACGACAGTCTGTGTCAGACCACTATCAGGAGGAGGCCAGGAG	597	
Qy	1473	gggcccggcctagagagagacagagcaacagagagctccctgcgcccagcagcagcggccgg	1532	
Db	598	GTCCAGGCTTGAGAGGAGGAACACGAGAGTCAAGGACCCCGTAGCCGGAAGACACAGCGGG	657	
Qy	1533	aggcacaccctggccgagagcttccaccccgctctcc	1568	
Db	658	AGGCACACATATGAGCTGAAGAGTCTCCAGCATTTC	693	

RESULT	4
AK017789	
LOCUS	
DEFINITION	AK017789 2411 bp mRNA HMC 05-JUL-2001
ACCESSION	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730525022, full insert sequence.
VERSION	AK017789.1 GI:12857214
KEYWORDS	CAP trapped.
SOURCE	Mus musculus (Strain:C57BL/6J) 8 days embryo cDNA to mRNA,

ORGANISM
Mus musculus
clone: 5730525022.

REFERENCE
1 (bases 1 to 2411)
Eunatayola, Metazoa: Chordata; Cranialta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
JOURNAL
Methods in enzymology. 303, 19-44 (1999)
MEDLINE
98272925
PUBMED
10349636

AUTHORS	TITLE	JOURNAL	PUBMED	MEDLINE	REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Suganuma, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome research. 10 (10), 1617-1630 (2000)	20499374		
			11042159		
	3 (bases 1 to 2411)				
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, T., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A., Yamamoto, S., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujimoto, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexillary sequencer	Genome research. 10 (11), 1757-1771 (2000)			
JOURNAL					
MEDLINE					
PUBMED					
4 (bases 1 to 2411)					
The RIKEN Genome Exploration Research Group Phase II Team and the					

1

Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MGS-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038

	BASE COUNT	87 a	157 c	107 g	88 t	
	ORIGIN					
	Query Match	10.4%; Score 273.8; DB 10; Length 439;				
	Best Local Similarity	78.3%; Pred. No. 1e-28;				
	Matches 342; Conservative	0; Mismatches 92; Indels 3; Gaps 1.				
Oy	1209	cggcttgagatcgtgacactcaagtgttttgaagtgctcagaaggtcttcaccaggac	1268			
Db	5	CAGCTCCCAAGCTCAGACCTCGACGTCGTGGAGGTTCTTCAAGAAATTCCTCCGTTGTAC	64			
Oy	1269	cccttcgcaccctgccttgtcgtcccgaagcgagacctgtgtgacgcgtctccag	1328			
Db	65	CCTTTCCGGCCCCCTCTCTGCTGTGTCACCACAGCCCCAGGCGCTTGCTCAGTCTCTGCAG	124			
Oy	1329	gccgagatgatcgtgagatccaagacccctgcgtcagtagtgccttgtcttcaccgttgat	1388			
Db	125	GCTGAGATTAGACTGTGATCTCCACAGCTCACACTCA---GCCCTATTATTATCCCCTGGATT	181			
Oy	1389	gccagctgcagcggagtglttcgcgcccgccccgtgtccccaagcagcctgtctgacaca	1448			
Db	182	ACCAACTCATGATGGAGTGTTCGGGACCGAATTCATCTCCCAAGCAGTCTGTGGACACA	241			
Oy	1449	gccatacatgtgaggagccaaagcagagggcccgccctaaggagagagagacagcagagag	1508			
Db	242	GCTATTCACCGAGGAGCGCCAGCGAGGTTCCAGCCATTATAGGAAGAAGAGGTCTCAGGA	301			
Oy	1509	tccctgcaccagcagcagggcgccgagagacacacctgcgcagagtctcacccgccttcc	1568			
Db	302	CCCCGCCCCGGAAGACACAGGCCGGAGGACACATTGGCTGAAGTCTTCAACCATTTCTCC	361			
Oy	1569	ccactcacgcgcacatgatatagtcgtctccctccaccacagcgcaagtcctgtcagaagga	1628			
Db	362	CCGGTCACACCTCTCTGATTAATTGTCTCTCCTGTGCACGCGGAGTCCCTCGGAAGGG	421			
Oy	1629	accagctctgacagtgtg	1645			
Db	422	ACCACTCTCGACAGCTG	438			
RESULT	9					
LOCUS	AV612708	586 bp	mRNA	EST	30-AUG-2000	
DEFINITION	AV612708 Bos taurus lung fetus Bos taurus cDNA clone EILU047B05 5'					
ACCESSION	AV612708					
VERSION	AV612708.1	GI:9748378				
KEYWORDS	EST.					
SOURCE	COW.					
ORGANISM	Bos taurus					
REFERENCE	Eumalvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 586) Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and Suzuki,H.					
TITLE	bovine cDNA sequencing					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Yoshikazu Sugimoto Animal Genetics Division Shirakawa Institute of Animal Genetics Odaoka, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan Tel: 81-248-25-5641 Fax: 81-248-25-5725 Email: kazusugie@ocn.ocn.ne.jp Single pass sequencing. This clone was obtained from a polyA-deleted cDNA library. Location/Qualifiers 1..586 /organism="Bos taurus" /db_xref="taxon:9913" /clone="EILU047B05"					
FEATURES	source					

[illegible]

Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LNCM792 row: e column: 03
 High quality sequence stop: 751.

FEATURES

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 /tissue_type="small cell carcinoma"
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 226 a 162 c 189 g 186 t
 ORIGIN

Query Match 10.1%; Score 267; DB 11; Length 763;
 Best Local Similarity 61.1%; Pred. No. 7.2e-28;
 Matches 449; Conservative 0; Mismatches 285; Indels 1; Gaps 1;

235 tcgcggttgatgaagtcgagcgatcgatccacaaacgaggttcgaataaataa 294
 1 tttccaaagctgaattggtcccccacacatctgacgaagagtgatgacatga 60
 295 ttgataaaacagattagttcaagcaatttggagaataatcatcgtagtcaagc 354
 61 ttgacaaagctcaacgaagctctccacgctccagaaactatcccggaagataa 120
 355 tgaagcttcgaacatcacatcatatagaagctttacaggttatgagaacaagaca 414
 121 tgaaggttttgatgaatcccaacatgatttaattttgaagtgatgacgacaa 180
 415 tgccttaacatcgatcgaatttgcctaaatgaggaatgtttgattatltga 474
 181 cgcttacctgtgcatgagtgagtgacgagagagagattttgatttacctag 240
 475 acgggacactgtagaagcagcgaggaagaagttctgcgaatccgtcgccgtg 534
 241 atggcagagtgaaagaaagagctcgagccaaattccgcagatagtgctgtgc 300
 535 agtactgtcaacatcacatcgctccacggagacccaagacccctcgtcg 594
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 655 agccctgtccacgctggtggagagcccccgtatgcccggcggagagcttgg 713
 421 acaacctggacaccttctgtggaagctcccttattgctcccaaaactcttc 480
 714 aagagatagaagcccccagctgacatctgagccctggaggtgtgtgtgtaag 773
 481 aaaaaattatgatgacacccagctgagtgatgtgagacctaagcattatct 540
 774 gtctcggttctcctcctcgtatggcctaaccctgcagcctgagacagcggt 833
 541 gtacacgcatccctcttcttattgatgacaaacctaagacactcgaggag 600

QY 834 gaaggcccttcgcgcatccctcttcacatgtcgaagactgtagagccgtatccgcgc 893
 DB 601 acgggaaatattccgtattctacattctacacgacgtgaaacactgcttaagaaa 660
 QY 894 atgctgtgtgtgaccccgccagcgacatcacatgtccagatccgcagccggtg 953
 DB 661 tttctcatcttattatccacagacagacgactttgagcaaatcatgaaatgatgc 720
 QY 954 atgagcgctgaagcc 968
 DB 721 atgaatgtgggtccc 735

RESULT 11
 BE900808
 LOCUS 601674532F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957366 5',
 DEFINITION mRNA sequence.
 ACCESSION BE900808
 VERSION BE900808.1 GI:10389353
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://mgi.mcl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LNCM834 row: p column: 07
 High quality sequence stop: 665.

FEATURES

source
 1..677
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3957366"
 /clone_lib="NIH_MGC_21"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: placenta; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 231 a 130 c 147 g 169 t
 ORIGIN

Query Match 10.1%; Score 265.4; DB 11; Length 677;
 Best Local Similarity 62.1%; Pred. No. 1.3e-27;
 Matches 419; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 283 caataaaataatgataaacaagatagatcaagcaatttggagaataatcatcgtg 342
 DB 1 CATATAAATATTGACAAACACTGTAATTCACAAAGTCTACAAAGCTTTCAGAG 60
 QY 343 aggttcagctgtagaagcttcgaacacacacacataaagcttaccagttatgg 402
 DB 61 AAGTAAGATTAATGAAGATTTAAATCAATCAATTAAGTAAGTATTCGAAGCATG 120
 QY 403 aaacaaaggaatgcttcatcgcgtcaacttgcctaaataatggagaatgttgatt 462

Db 121 AAGTCAAAAAACCTCTACCTATCATGTAATGCAAGTGAAGTATTGACT 180
Oy 463 attgacttccacgagccactgagtagaagcggagcggaagagttctggcaatcc 522
Db 181 ATTGGTTGCACATGACGAGATGAGCAAAAAAGCAACAGATCTAATATTAGACAGATTG 240
Oy 523 tctggcgctgagtagctgtcaacgacatcaatcgltcaacggagaccccaagaacgaga 562
Db 241 TCTCTGCACTTCAATATCTCCATCAGAAACGGATCTACATCAGACCTCAAGCTGAAA 300
Oy 583 acctctgtgtgtagcaacatgacatgaagctgacatgttggatttggagatttct 642
Db 301 ATCTATTGTTAGATGCCGATATGAAATACATTAATACAGATTCGGTTTACCAATGAAT 360
Oy 643 acaagtcagagagagcctctgtcaacgtgggtgagagcccccgtatgcccgcggaggaag 702
Db 361 TTACTGTTGGCGGTAACTGACACAGCTTTCGTGGACAGTCTCATACGACACCTGAGC 420
Oy 703 tcttgaagggagagagtagtgaagcccccagctgacatctgagagcctggcggtgtgc 762
Db 421 TCTTCCAGGGCAAGAAATATGACGGCCAGAAAGTGATGTGAGTCTGGCGTCAATT 480
Oy 763 tctagctctgtgtgagcttctctcccttgtagtgagcctaaccctgagcagctgagac 822
Db 481 TATACACTAGTCACTGCTCCTCACTTCCCTGATGGCAAAACCTTAAGAACTGAGAG 540
Oy 823 agcgggtgtctgagagcgccctccgcatccctctctcatgtctcaagactgtgagagcc 882
Db 541 AGGAGTATACAGAGGGCAATACCGAATTCCTCTACATGTCTACAGATGTGGAAGACC 600
Oy 883 tgatccgagcatgtgtgtgtgagaccccgagcgagcatcaccatcgcccgagatccggc 942
Db 601 TTCTCAACGTTTCCGTGCTAAATCAATTAACGGCGGCACTCTAGAACAAATCATGA 660
Oy 943 agcaccggtgagatgc 957
Db 661 AGGACAGGTGATCC 675

RESULT 12
LOCUS A1528387 435 bp mRNA EST 18-MAR-1999
DEFINITION U196h01.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1890289 5', mRNA sequence.
ACCESSION A1528387
VERSION A1528387.1 GI:4442522
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 435)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Smaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:974613
Seq primer: custom primer used
High quality sequence stop: 429.

FEATURES
source 1.435
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890289"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTG); Site_2: DraII (CACCATGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTG, 3' site CACCATGG). XhoI should
be used to isolate the cDNA insert. Site selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTTAAAGCTGG and 3' end
primer CGACGTGACGTCGACACA."
BASE COUNT 80 a 150 c 125 g 80 t
ORIGIN

Query Match 9.98; Score 261.6; DB 10; Length 435;
Best Local Similarity 76.6%; Pred: No. 4.9e-27;
Matches 334; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

Oy 1591 tctctccctccacagcggaagctctctgagaggaacagctctgacagttgtctga 1650
Db 2 TTGCTCTCTCTCTGCGACGCGAGTCCCTCGAAGGACCAAGTCCGACAGCTGCTCC 61
Oy 1651 cctctctcgagcaaaaagcccgcgaggtcagltgaccccgccactcaaggggtgc 1710
Db 62 CTTTCTGCAAGTGAAGGTCCTGACAGGCTTGACAGTGGCTGGCCACCCAGGCGTGC 121
Oy 1711 tgggagctgtctcccgagtagagctgtgctccctctcgagggtcgagtcgcaacc 1770
Db 122 TGGGCAACCACTCTCCAGTGAAGATTGGCTGCGCTTCTGGAATCAAGTCAACACC 181
Oy 1771 cagtgctcagagctcaaggggagctggagagagctgtctcctccgtcagctccagg 1830
Db 182 CTGTGCTCCAGACTCAGGCAAGTGTGGGACACAGCCGCTTACCTCCGCTTCCAGG 241
Oy 1831 agggacggcgagctcgagacactcactgactcaagagctgaaagccttctggcagcag 1890
Db 242 AGGAGCGGAGAGGCTCTGATACCTCTCTCACTCAGGGGCTGAAGGCTCCGGACAGC 301
Oy 1891 tgaagaaagaccagcgagcaaaaaggttcttggagctgaaacaaatcaagggctgctc 1950
Db 302 TGAGGAAAAATGCGAGGAGCAAGGGGTTCTCGGAGACTGACAAAGTAAAGGTTGGCTC 361
Oy 1951 gccaggtgttccagagctccctcgccagcgcgagcagggcgagctgagccctcagc 2010
Db 362 GCCAGGTGTGCGA---TCTCTCCGTCGGAACCTCCCGGGAGGATGATGACTTCCACA 418
Oy 2011 cccctgacagagccc 2026
Db 419 CCCAGCCCCCAAGCTC 434

RESULT 13
LOCUS AUI32239 866 bp mRNA EST 24-OCT-2000
DEFINITION AUI32239 NT2RP3 Homo sapiens cDNA clone NT2RP304052 5', mRNA
sequence.
ACCESSION AUI32239
VERSION AUI32239.1 GI:10992593
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Search completed: March 22, 2002, 12:15:06
Job time: 5304 sec

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Db 1741 cgcctctctctgggttcgacagtcgccacccacagtcgtcagagctcagggggtctggag 1800
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Oy 1861 ctcaagggcgaagggccttcgcgacagcttgaggaagacacgacgagccaaaggtcttc 1920
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Oy 2461 tccctgagcagtgagggcagccctcgtacacacacacacacacacacacacacacacac 2520
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Db 2521 ctccagagagggatgagacacacacacacacacacacacacacacacacacacacacac 2580
Oy 2581 caatacgtatggtgttcttgccgaaataataataataataataataataataataata 2632
Db 2581 caatacgtatggtgttcttgccgaaataataataataataataataataataataata 2632
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RESULT 2

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AAx82951
ID AAx82951 standard; cdna: 2533 bp.
AC AAx82951:
XX 07-JUL-2000 (first entry)
XX Human keratinocyte derived pKer122 encoding cdna #1.
DE
XX
```

```
KM Keratinocyte: regulatory protein; human: pKer122; antiproliferative;
KW kinase; signal transduction; desmosome; dermatological condition.
KM pemphigus vulgaris; psoriasis vulgaris; epidermis; cosmetic; ss.
OS Homo sapiens.
PN WO200017232-A2.
PD 30-MAR-2000.
XX
PF 06-SEP-1999; 99MO-DE02865.
XX
PR 19-SEP-1998; 98DE-1042863.
XX
PA (KRAM/) KRAMER M.
PI Kramer M, Bechtel M, Reinartz J, Schaefer B, Wallich R;
XX
DR WPI; 2000-283542/24.
DR P-PSDB; AAW90878.
XX
PT New regulatory polypeptide from keratinocytes, useful for diagnosis and
PS treatment of dermatological disorders, also in cosmetics
PS Claim 2; Page 49; 55pp; German.
XX
CC This invention describes a novel human regulatory polypeptide designated
CC pKer122 (I), or its variants from human keratinocytes, which in activated
CC keratinocytes is the same as, or similar to, the most highly expressed
CC protein and has antiproliferative activity. (I) is a kinase involved in
CC signal transduction and is conjectured to be involved in cell-cell or
CC cell-matrix interactions and/or formation of (hem)desmosomes. Modulation
CC of (I) will affect proliferation and differentiation of keratinocytes.
CC (I) is upregulated in some dermatological conditions, e.g. pemphigus
CC vulgaris and psoriasis vulgaris. (I) is used to raise specific antibodies
CC (Ab) which are used for diagnosis and treatment of dermatological
CC disorders and for cosmetic treatment of the epidermis. Nucleic acid (II)
CC that encodes (I) is used: (i) to produce transgenic mammals (particularly
CC mice and rats); and (ii) as source of sense and antisense
CC oligonucleotides for diagnosis and treatment of dermatological disorders
CC and for cosmetic treatment of the epidermis. (II), (I) and polypeptides
CC (Ia) produced by splice variants of (II) are used to identify specific
CC binding agents (potentially useful in medicine and cosmetics) that
CC modulate their function and/or expression, especially inhibitors and
CC activators. Cells and animals transformed with (II) are used to study
CC (i)-induced changes in cell morphology and basic functions. This
CC sequence encodes the human keratinocyte protein pKer122 described in the
CC method of the invention.
XX
SQ Sequence 2533 BP; 501 A; 820 C; 762 G; 450 T; 0 other;
XX
Query Match 95.9%; Score 2522.8; DB 21; Length 2533;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 8 aggtgcgacgagacatgtatcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 166
Oy 167 tcaaggcagcagaagaatccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 226
Db 68 tcaaggcagcagaagaatccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 127
Oy 227 aggtcaactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 286
Db 128 aggtcaactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 187
Oy 287 aaaaataatgataaaacacacacacacacacacacacacacacacacacacacacacacac 346
Db 188 aaaaataatgataaaacacacacacacacacacacacacacacacacacacacacacacac 247
Oy 347 tcaagctatgaagcttctgaacacacacacacacacacacacacacacacacacacacacac 406
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|||||
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QY 407 aagagacatgcttaccatcgtacatgtaatttgctaaataatgagaaatgcttgattatt 466
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Db 308 aagagacatgcttaccatcgtacatgtaatttgctaaataatgagaaatgcttgattatt 367
QY 467 gaattccaaacgggacacatgagtgagaaacgagcgcgagaaagatctctgcaaatccctgc 526
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Db 368 gaattccaaacgggacacatgagtgagaaacgagcgcgagaaagatctctgcaaatccctgc 427
QY 527 ggcgcgtgagatcttaccagacatcgtaccacgggagacccccaagacccaagacaaact 586
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Db 428 ggcgcgtgagatcttaccagacatcgtaccacgggagacccccaagacccaagacaaact 487
QY 587 cctgctgagatgagcaacatgagacataaagctggcagaaatttggaatttggaatttccaa 646
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Db 488 cctgctgagatgagcaacatgagacataaagctggcagaaatttggaatttggaatttccaa 547
QY 647 gtcagagagagcctctgttccacgttggtgtagagaccccccgtatgacggcccggaagctct 706
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|||||

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Db 1748 ggaacacatcagatcacaagagctgaaagacattctcgagcagacgtgaaagacacacgcg 1807
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QY 1967 cccctgcagagcgggcccagacagggcgagcctgagagcccttccacgcctctccacagagccc 2026
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|||||
Db 1928 aagcctgcagagcgggcccagacagggcgagcctgagagcccttccacgcctctccacagagccc 1987
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Db 1988 agbagaagcagagagctgctccacaggttaacagacacacggcgctgcacacggcgcttccca 2047
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Db 2228 caacggcccccaacggcctcccgctgtgtccccaacacagccttggacaggtctgcgccaag 2287
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QY 2507 tcttaagcaataactctcagagaggtgaagacatcttgagcctcaaaagccaagaaacttct 2566
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Db 2408 tcttaagcaataactctcagagaggtgaagacatcttgagcctcaaaagccaagaaacttct 2467

OY	2567	agaaacggaatcgaatcagcttaagctgttttggcgaaaaa	2626
DB	2468	agaaacggaatcgaatcagcttaagctgttttggcgaaaaa	2527
OY	2627	aaaaa 2632	
DB	2528	aaaaa 2533	
<p>RESULT 3</p> <p>AA06718 standard; cDNA: 2361 BP.</p> <p>AA06718:</p> <p>12-SEP-2001 (first entry)</p> <p>Polynucleotide sequence encoding human protein kinase #18.</p> <p>Human; protein kinase; PK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.</p> <p>Homo sapiens.</p> <p>WO200138503-A2.</p> <p>31-MAY-2001.</p> <p>22-NOV-2000; 2000WO-US32085.</p> <p>24-NOV-1999; 99US-0167482.</p> <p>(SUGEN-) SUGEN INC.</p> <p>Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R; Flanagan P, Clary D;</p> <p>WPI: 2001-343950/36.</p> <p>P-PSDB; AAU03518.</p> <p>Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -</p> <p>Example 1: Figure 1; 433pp; English.</p> <p>AA06701-AA06757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PRK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.</p> <p>The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.</p> <p>Sequence 2361 BP: 431 A; 784 C; 726 G; 420 T; 0 other;</p>			
Query Match	88.4%	Score 2326.6;	DB 22; Length 2361;
Best Local Similarity	99.4%	Pred. No. 0;	
Matches 2348; Conservative	0;	Mismatches	4; Indels 9; Gaps 1;

OY	123	a t g t t a c a t g t c g a g t l t c a g c g y g a c c c g y g c c a a g t c a g g t c a g g c a g a a g	182
D b	1	a t g t t a c a t g t c g a g t l t c a g c g y g a c c c g y g c c a a g t c a g g t c a g g c a g a a g	60
OY	183	t c c c c c g g g t g g g t t t t a c g a t c g a g c g a g g a c c t t g g c a a a g c a a c t t c g c g t g	242
D b	61	c c c c t c g g g t g g g t t t t a g a c a t c g a g c g g c c t t g g c a a a g c a a c t t c g c g t g	120
OY	243	g t g a a g c t g c g y g a t c g a g t c a c c a a a c g c a g g t t g c a a t a a a t a t g a t a a	302
D b	121	g t g a a g c t g c g y g a t c g a g t c a c c a a a c g c a g g t t g c a a t a a a t a t g t a a a	180
OY	303	a a c a g a t t a g a t t c a a g a c a a t t t g g a g a a a t c t a c t g t a g g t t c a g c t g a g a g c t t	362
D b	181	a c a c g a t t a g a t t c a a g a c a a t t t g a g a a a a t c t a c t g t a g g t t c a g c t g a g a g c t t	240
OY	363	c t g a a c c a t c c a c a t c a t a a a g c t t a c c a g t t a t g a a a c a a g a g a c a t g c t t a c	422
D b	241	c t g a a c c a t c c a c a t c a t a a a g c t t a c c a g t t a t g a a a c a a g a g a c a t g c t t a c	300
OY	423	a t c g t c a c t g a a t t g c t a a a a t g g a g a a t g t t g a t a t t t g a t t t g a c t t c c a a g y g a c	482
D b	301	a t c g t c a c t g a a t t g c t a a a a t g g a g a a t g t t t a t t a t t g a c t t c c a a g y g a c a c	360
OY	483	c t g a g t g a a c a g a a g c g c g a a g a a d t t c t g g a a a t c c t t g c g c g y g a g t a c t t	542
D b	361	c g a g t g a a c a g a a g c g y g a a a a g t c t c g a a a t c c t g c g c g y g a g t a c t t	420
OY	543	c a g a c c a t c a c a t c g t c c a c c g y g a c c t c a a g a c c t c a a g a c c t c b t c y t a g t a g a a c	602
D b	421	c a g a c c a t c a c a t c g t c c a c c g y g a c c t c a a g a c c t c a a g a c c t c b t c y t a g t a g a a c	480
.OY	603	a t g g a c a t c a a g c t g b g c a ----- g a t t t g a t t t g g a a t t c t e a a g t c a a g a	653
D b	481	a t g g a c a t c a a g c t g b g c a g a c a g a a g a t t t g a t t t g g a a t t c t e a a g t c a a g a	540
OY	654	g a g c c t c t g t c c a c a g t g t g t g g a g c c c c c g t a t a g c c c c c g a a g t c t t t g a g g	713
D b	541	g a g c c t c t g t c c a c a g t g t g t g g a g c c c c c g t a t a g c c c c g a a g t c t t t g a g g	600
OY	714	a a g a g t a t g a a g c c c c a a g c t g a a c a t c t g a g a c c t t g g c g t t g t g c t g t a c g t c c g	773
D b	601	a a g a g t a t g a a g c c c c a a g c t g a a a c t c t g a g a c c t t g g c g t t g t g c t g t a c g t c c g	660
OY	774	g t c t c g a t t c t c t c c c c t t a g t a t g a t c c a c c t c g a c c g t c t g a a c a g c a g c g g t g c g	833
D b	661	g t c t c g a t t c t c t c c c c t t a g t a t g a g c t a a c c t g c a g a c g t c t g a a c a g c g g t g c g	720
OY	834	g a g a g c c g t c c g a c a t c c c t c t c a t g t c t c a a g a c t g a g a g c t g a t c c g a c	893
D b	721	g a g a g c c g t c c g a c a t c c c t c t c a t g t c t c a a a g a c t g a g a g c t g a t c c g a c	780
OY	894	a t g c g t g t g g t g a a c c c c g a a g c g a t a c a a c a t c g c a a g a t c c g a g a c c g g t g g	953
D b	781	a t g c g t g t g g t g a a c c c c g a a g c g a t a c a a c a t c g c a a g a t c c g a g a c c g y g t g	840
OY	954	a t g c g a g t c t g a c c c t g t c g a g a c c c g a c c t g c c c g c t t c t c g a c a a g a c t a c	1011
D b	841	a t g c g a g t c t g a c c c t g t c g a g a c c c g a c c t g c c c g a c t t c t c g a c a a g a c t a c	900
OY	1014	a c c t c a a c c t g g g c g a t a g a t g a a c a a g c g c t g g g t a t a t g a a g c c t g g g c g t g	1077
D b	901	a c c t c a a c c t g g g c g a t a g a t g a a c a a g c g c t g g g t a t a t g a a g c c t g g g c g t g	960
OY	1074	g a c c g c a g a g a c g t g a g a t c a c t c a a a a c a g a c a g c t a t a a c a c a t t g c t g c a t t	1133
D b	961	g a c c g c a g a g a c g t g a g a t c a c t c a a a a c a g a c a g c t a t a a c a c a t t g c t g c a t t	1021
OY	1134	t a t t a c c t c c t c t g a g c g a t a a g a g a t a t c g a a t a g c c a g t g c g c c g c c c g g g	1193
D b	1021	t a t t a c c t c c t c t g a g c g a t a a g a g a t a t c g a a t a g c c a g t g c g c c g c c c g g g	1080

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D02221	cccaacgcctcccgctgtgcccacacacgccttgccagagctgtgcccagattgttag	2280
QY2394	ccctcggagctgctgcagagggagactgtgagatggagagacctatgcccctgctccctaac	2453
D02281	ccctcggagctgctgcagagggagactgtgagatggagagacctatgcccctgctccctaac	2340
QY2454	acgtttgtcctggtgcagtga	2474
D02341	acgtttgtcctggtgcagtga	2361

RESULT 4

ID AACC68862 standard; cDNA; 640 BP

AC AAC68862;

DT 21-FEB-2001 (first entry)

Human protein fragment PN7065 coding sequence SEQ ID NO: 3.

KW Protein-protein interaction; physiological disorder; NIDDM;
KW neurodegenerative disorder; drug screening; predisposition;;
KW non-insulin dependent diabetes mellitus; ss.

OS Homo sapiens.

PN WO200065340-A1.

PD 02-NOV-2000.

PF 21-APR-2000; 2000WO-US10651.

PR 22-APR-1999; 99US-0130389.

PR 30-SEP-1999; 99US-0156947

PR 02-DEC-1999; 99US-0168376.

[illegible]

XX
XX

XX 2000-607376 457

DR P-PSDB; AAB36283.

Novel protein complexes involved in mammalian physiological pathways,

PT Alzheimer's disease, and in drug screening for identifying modulators of

XX 01:47: 0700: Escalab
XX 01:47: 0700: Escalab

[illegible]

CC are involved in mammalian physiological diseases and disorders. These include non-insulin dependent diabetes mellitus (NIDDM) and

CC neurodegenerative diseases such as Alzheimer's disease. The protein CC can be used in the diagnosis of these diseases and a

CC predisposition to them, in drug screening and in the identification of other proteins involved in the same pathway.

XX 640 pp. 104 A. 220 C. 202 C. 106 F. 0 other

Query Match
Post 10001

Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy	945	caaccggtgagatgctgagtgcccttgctgacggagcccgctgcccgcctctctccgca	1004
Db	1	cgccgggtgagatgctgagtgccctctgtccgggagcccgctgcccgcctctctccgca	60
Oy	1005	caacgctacacctcccaacccctgggcagactaagatgagacagcgctggtatctatgaagac	1064
Db	61	caacgctacacacctcccaacccctgggcagactaagatgagacagcgctggtatctatgaagac	120
Oy	1065	ctggcgctggagccgagcagagctgagagtcactctgcaaaaacagacgactataaccactt	1124
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Oy	1185	cgccccgagcctgtccagagcagcgcgcctccagagctctgagactcagtggtttgaggtg	1244
Db	241	cgccccgagcctgtccagagcagcgcgcctccagagctctgagactcagtggtttgaggtg	300
Oy	1245	ccctaaagaaaggtctcttcacacgaccccttcacgaactgtgctgtgcccagcgcag	1304
Db	301	ccctaaagaaaggtctcttcacacgaccccttcacgaactgtgctgtgcccagcgcag	360
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Db	361	accttggctgcaagttccgctccctccagagcagagatgactgtgagctccaaagctcgctgacg	420
Oy	1365	tggccctctgtctctcccggtgagatgacagctgagagagtgcttccgagcccgagcctg	1424
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Oy	1425	tccccaagcagcctgtctgtgacacagccatcagtgtgaagagccagacagggccgggctcta	1484
Db	481	tccccaagcagcctgtctgtgacacagccatcagtgtgaagagccagacagggccgggctcta	540
Oy	1485	gaggagaagagcagagacagcagaggtcccttgcccagacagacggccggagagacacccctg	1544
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Oy	1545	gccgaaggtctccacaccgcgcctctcccaactaacgcgcga	1583
Db	601	gccgaaggtctccacaccgcgcctctcccaactaacgcgcga	639
RESULT 5			
AAFA4658			
ID	AAFA4658 standard; cDNA; 5163. BP.		
XX	AAFA4658:		
XX	27-MAR-2001 (first entry)		
DE	Novel protein kinase cDNA, SEQ ID NO: 38.		
XX	Human: mouse; protein kinase: antiarthritic; antisclerotic; osteopath		
KW	immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;		
KW	dermatological; antidiabetic; antifertility; gene therapy; vaccine;		
KW	immune disorder; cardiovascular disease; neurodegenerative disease;		
KW	cancer; autoimmune disorder; stroke; inflammatory bowel disease;		
XX	inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.		
OS	Homo sapiens.		
PN	MO200073469-A2.		
XX	07-DEC-2000.		
PD	26-MAY-2000; 2000MO-US14842.		
EP	28-MAY-1999; 99US-0136503.		
XX			

[illegible]

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QY 694 ccccggaagctcttgagggaagatgaagcccccagctgtgacatctgagcctgg 753
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DB 705 ccccggaagctcttgagggaagatgaagcccccagctgtgacatctgagcctgg 764
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 754 gctgtgtgtgacgttcctgcgtgcgtgtctcccttcgattgagcctgaaccgcga 813
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 765 gactgtgtcttattgtctctgtctgtgagcctgccttcgttgaagccgactcttcaa 824
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 814 cgcctgagacgctgtgtctgagggccgcttcgcagatcccttccttcatgtctcaagct 873
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 825 ttcttgagagagaggtgtctcgagaagatctccgattccgatttcatgtcagaagatt 884
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 874 gctgagagcctgtatccgcgcgcgtgtgtgtgagcccgccgagcgcatccaccatccgc 933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 885 gctgagacacttaccgaagatgtgtgtctcctagaccatcccaacgagtaaccatagccc 944
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 934 agatccgcgagacgctgtgagatgcggtgtgagccctgtcttcgagccgctgtccccc 993
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 945 aatccagagagatgaatgagatgtctcatagagttccctgtccagagacctgttctctatc 1004
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 994 ccttctccgacacagctacactccactccactgtggtgacatgagcagcgctgggta 1053
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1005 cacaagagcaagaataatgagccatcca---tcggggagtttaatgagcggttctgcgac 1061
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1054 tcatgacagaccctggtggtgcgtgcgacgagagagcggtgagctcaacacagcagcgt 1113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1062 tgatgacagcctgtggaatagatcagcagaaraacatgtgacttgcagacaagagct 1121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1114 ataacacattgtgcacattattacccctcctctgagcgcgtcagaagatctcga 1170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1122 ataaccacttgcgtccatttattcttctgtgtgtgagcgctggaatcaccatcgga 1178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 6
AAFA4652
ID AAFA4652 standard; CDNA; 4321 BP.
XX
XX
AC AAFA4652;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase cDNA, SEQ ID NO: 32.
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200073469-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 26-MAY-2000; 2000MO-US14842.
PE
XX
XX 28-MAY-1999; 99US-0136503.
PR
XX
XX (SUGEN-) SUGEN INC.
PA
XX
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
PI
XX
XX MPI; 2001-032161/04.
DR
XX
XX P-PSDB; AAB65626.
PT
XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
XX
PS Example 1; Fig 2; 310pp; English.

XX
CC The present sequence encodes a novel protein kinase. The nucleic acids
CC and the protein kinases they encode may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
CC
CC
XX
S0 Sequence 4321 BP; 1074 A; 1279 C; 1087 G; 881 T; 0 other;

Query Match 14.5%; Score 382.6; DB 22; Length 4321;
Best Local Similarity 61.7%; Pred. NO. 1.4e-64;
Matches 629; Conservative 0; Mismatches 384; Indels 6; Gaps 1;

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QY 148 cggaccgcggcgccagagtcagggccagagaagctccctcgggtgtgttttacgaca 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 114 cgcgtcccccagcccccgcctccctcccgagccatgcgcgcgcgtatcgtctactcaga 173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 208 tcgagcagaccctgggccaaggaacttcgcgtgtgtgtgaaagctgcgcgcgcatctga 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 174 tcgaccgcacatcgcgcaagggcaacttcgcgtgtgtgtgaaagcgggccaagcactctga 233
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 268 ccaaaacgcaagtgcgaataaataatgataaacaagatgatccaagcaatttg 327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 234 ccaagcccaaggtgtgtctcaagatcagataagataagccacgtgtgaaagaaacttga 293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 328 agaaatctatcgttgaggttcaagctgataagagcttctgaaacatccacatcaataaagc 387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 294 agaagatttccgggaagtccaattatgaagatgcttgcaccccatactacagc 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 388 ttaccaggttatggaacaagaagacatgctttacatcgttcacgaatttgcataaagt 447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 354 tctaccaggttatggaacaagaagacatgctttacatcgttcacgaatttgcataaagt 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 448 gagaatgttgatatttgacttccaagggcaccctgagtagaagagagcgcggaaga 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 414 ggaataatttgaccacccctgtgcccacatgtagaatgtagaagagggcagctcga 473
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 508 agttctggcaaatcctgtcggcgtgtgagttactgtcacgaccatcacatcgtccacggg 567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 474 agttcaaacagatcgtlccacagctgtctatttctgacctgtcggaaacattgtatccgt 533
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 568 accccaagacgcgaagacctcctgctgtagtggaatggaatgacatcaagctggcagatttg 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 534 atttaaaagctgaaaatttacttctcgtgacatctgaaatcaataaataagcagatttg 593
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 628 gatttgggaattctacaagtcagagagcctctgtccacgtgtgtgtgtgtggagcccccgt 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 594 gtttcagtaaccttcaactcctgtgagcagctgtcgaagacctgtgtgtgacgacctccct 653
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 688 atgcgcgcccggaagctcttgaggggaaggtatgaagagcccccagcttgacatcttga 747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 654 atgctgcacacttgaaactcttgaaagaaagataagatggtggcgaacatccttga 713
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 748 gctctgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 714 gctctgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 773
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 808 tgcagacgttgagacagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 867
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 774 tgcagatctgtggcgccgctgctgagtggaagttccgcgatacccatcttattatgtcca 833
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 OS Homo sapiens.
 XX
 XX WO200073469-A2.
 PN
 XX 07-DEC-2000.
 XX
 PD 26-MAY-2000: 2000WO-US14842.
 XX
 XX 28-MAY-1999: 99US-0136503.
 PR
 XX (SUGEN-) SUGEN INC.
 PA
 XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
 PI WPI; 2001-032161/04.
 DR P-PSDB; AAB65628.
 XX
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 XX
 XX Disclosure; Fig 2; 310pp; English.
 PS
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 CC
 SO Sequence 2190 BP; 709 A; 484 C; 504 G; 493 T; 0 other;

Query Match 10.8%; Score 285.4; DB 22; Length 2190;
 Best Local Similarity 61.3%; Pred. No. 6e-46;
 Matches 460; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 216 acccttgagcaaaagcacttcggtggtgaaagtgcgagcgtacgtacccaacg 275
 DB 181 acaatcgcaaggaggaatttcgcaaaagtaaatggaagacatccttcacagcaga 240
 QY 276 caagttgcaataaataatgtaaaacacgaattagatcaagcaattcgagaacatc 335
 DB 241 gaggttgcaataaataatgcaaaaactcagttgataccaagaatcctcaaaaagctc 300
 QY 336 taccgtgaggttcacgtgataagcttcgaaccatcacacatcataaagcttaccag 395
 DB 301 ttcagaggaagtgaagaataagattttaaatccatccaatagtagaagtattcgaa 360
 QY 396 gttatggaacaagaagacatgcgtttacatcgttcactgaatttcttaaaatgagaatg 455
 DB 361 gtcactgaaactgaaaaaacatctaccatcaatcagaaatagcaagtgagagta 420
 QY 456 ttgatatttcacgtccaaagcgacctgagtgaagacagcgcggaagaagttcttg 515
 DB 421 ttgactatttggtgcactgcgagatgagaagaaaaagaagcaagaatcttaattaga 480

QY 516 caaatctgtcgccgtgaggtactgtcaagacatcacatcgtccacgagacctaaag 575
 DB 481 cagattgtctgcagttcattcattcagcacaagaagatcgtlacatcgagacctaaag 540
 QY 576 accgagacctcctcgtgagctgcaaatgacatcgaagcttgccagatttgagttgg 635
 DB 541 gctgaaatctattgttagatgcgatatgaacataaataagatcttcggttttagc 600
 QY 636 aattctacaagtcagagagccctgtccacgtgtgtgtggaagcccccgtatgcgcc 695
 DB 601 aatgaattactgttgcgcgttaactgcagacglttgttgccagcttccatcagcaga 660
 QY 696 ccggaagctcttgagggaagagatgaaggccccagcttgacatctgagacctggcc 755
 DB 661 cctgagctcttcagagcaagaataatgacggccagaagtgtgagtgtctggg 720
 QY 756 gtgtgtgtgagcttcgtgcgttcgttcctcccttgatgagggcctaaccctgcagc 815
 DB 721 gtcatttatacaacactagtcagtgctcacttccttgcattgagggcaaaacctaaagaa 780
 QY 816 ctgagacagcgggtgctgagagggccgttcgcacatccctcttcattgtcagaagctgt 875
 DB 781 ctgagagagagagatataaagagaaatagagaattcctcttcacatgcttaagactgt 840
 QY 876 gagaagcttgatccgcgcgatgtgtgtgtgagcccgccagagccatccaccatcgccag 935
 DB 841 gaaaccttcataaagcttctcgtgtctaataatcaatcaaacgagcacttagagcaa 900
 QY 936 atccgcagcagccggtgagtgagcggtcagc 966
 DB 901 atcatgaagagcaggtgagatcatcagggc 931

RESULT 10
 AAV03002
 ID AAV03002 standard; cDNA to mRNA; 2698 BP.
 AC AAV03002;
 XX
 XX 18-JUN-1998 (first entry)
 DE Human Twenty-five C associated protein kinase 1 encoding cDNA.
 KW Human; twenty-five C associated protein kinase 1; TCAK1; detection;
 KW cancer; cell proliferation; Cdc25; phosphorylation; 14-3-3 protein; ds.
 OS Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 FH CDS 376..2565
 FT /*tag= a
 FT /product= "TCAK1"
 XX
 XX
 PN WO9801756-A1.
 PD 15-JAN-1998
 XX
 PF 03-JUL-1997: 97WO-US11721.
 XX
 PR 09-JUL-1996: 96US-0677298.
 XX
 PA (UNIW) UNIV WASHINGTON.
 PI P1wnica-Worms H;
 XX
 DR WPI: 1998-101198/09.
 DR P-PSDB; AAB37158.
 XX
 PT DNA encoding Twenty-five C Associated protein Kinase 1 - useful for,
 PT e.g. detecting cancers or disorders of cell proliferation
 XX
 PS Claim 2; Page 35-39; 75pp; English.

Sequence 3857 BP; 1126 A; 991 C; 920 G; 820 T; 0 other;

Query Match	10.6%;	Score 279.2;	DB 22;	Length 3857;
Best Local Similarity	60.6%;	Pred. No. 1e-44;		
Matches 458; Conservative	0;	Mismatches 298;	Indels 0;	Gaps 0;

[illegible]

RESULT	12
AAF85149	
ID	AAF85149 standard; DNA; 4790 BP.
XX	
AC	
XX	AAF85149;
DT	09-JUL-2001 (first entry)
XX	
DE	DNA encoding a dishevelled associated kinase (DAK) isoform DAKb.
XX	
KW	Dishevelled associated kinase; DAK; DAKa; DAKb; DAKc; cell proliferation;
KW	cancer; ss.
XX	

Homo sapiens.

aa	Key	Location/Qualifiers
FH		

FT	CDS
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
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97	97
98	98
99	99
100	100

product="dishevelled associated kinase (DAK) isoform

ET

AA
PN
W0200125408-A1.

XX
X

XX

PF 06-OCT-2000; 2000WO-US27899.

PR

PR 14-SEP-2000; 2000US-0661965.

PA (REGC) UNIV CALIFORNIA.

XX

F1 SUM 1, WILLIAMS DI,
XX

DR WPI; 2001-316169/33.

DN F-15952, 66050341.
XX

PT Novel isolated Di

PT

PT -

XY
DS

XX

CC The present sequence encodes dishevelled associated kinase (DAK)

CC

33

CC

33

CC

33

CC

333

CC

33

CC

XX 53

2

Sequence 4790 BP; 1519 A; 1179 C; 1078 G; 1014 T; 0 other;

Query Match	10.68;	Score 279.2;	DB 22;	Length 4790;
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OY	201	tacgaacatcgagcgagaccctgggcaaaaggaacttcgcggtgtgtgaagcttgcgcgggcat	260
Db	1618	taccaactcattaagaacgagatctcggaagggcaattttgcacaagttgtaaatctagcgaataac	1677
OY	261	cgagtcaccacaaagcgcggtttgcataaataattgataaagaacgacttgatccaagc	320
Db	1678	ctgcacctgtgcgaagaggtctgcacataagaatattggacaaagcccaactcaatcttgg	1737
OY	321	aatttgggaanaactctactcgttgaggttcagctgaagccttcgaaacatccacacatc	380
Db	1738	tcactacagaacactcttagagaggttagatataatgaagtgctgtgataccccaacata	1797
OY	381	ataaagcttccacggttatggaacaaagacatgctttaaactcgtctactgaattgct	440
Db	1798	gttaaatattgttccaaagtaatccaaacggaagaagacgtctcattctgtacttggaaatga	1857

KW neurological disorder; ss.
 OS Homo sapiens.
 PN WO200112670-A1.
 PP 22-FEB-2001.
 PF 10-AUG-2000; 2000WO-US21736.
 PR 13-AUG-1999; 99US-0148682.
 PR 20-SEP-1999; 99US-0154887.
 PA (HDMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, NI J;
 DR MPI; 2001-202858/20.
 DR P-PSDB; AAB71959.
 PT Nucleic acid molecules encoding 12 transforming growth factor-beta
 PT receptor polypeptides, useful for preventing, diagnosing and treating
 PT e.g. cancers, Parkinson's disease and diabetic retinopathy -
 PS Claim 1; Page 285-286; 31pp; English.

The present sequence is a nucleic acid molecule encoding one of 12 novel human transforming growth factor (TGF)-beta receptor polypeptides. The TGF-beta receptor polynucleotides and polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. Such diseases include immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease) and infectious diseases. The polynucleotides and polypeptides are also useful for promoting wound healing, regeneration and/or chemotaxis. The polynucleotides and their complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of protein expression and activity. The anti-TGF-beta receptor antibodies may be used to down regulate expression and activity and as diagnostic agents for detecting the presence of the polypeptides in samples.

Sequence 3200 BP; 727 A; 948 C; 831 G; 694 T; 0 other;

Query Match	8.6%	Score 225.6	DB 22	Length 3200
Best Local Similarity	56.2%	Pred. No. 2e-34		
Matches 445; Conservative	0	Mismatches 344	Indels 3	Gaps 1

QY 164 gactcagggccagcagaagctccctccgggtggtgttttaagacatcgagcgagccctggg 223

Db 16 gaagcgcgccacccacacagcaaaactctgcgaccgcgtacagatctccctgagagccctggg 75

QY 224 caaagcgaacttcggcggtgtgtgaagcttgcgcggcgcgcatcgagtcacacaaaacgaggttgc 283

Db 76 caaagcgacctctcgggaaagtgtgaagaagcgcgggagagctccggcgcgctgttgccat 135

QY 284 aatlaaataatctgataaacaacgactgattcaagcaatttggagaatactatcgta 343

Db 136 caagtcaatccggaagacaataatcaagaatgtgagcaagatctgtatgcatactcggagtgga 195

QY 344 ggttcgcgtgatgaagctcttgcacacatccacacataaagctttaccaggttaaggga 403

Db 196 gatttgagatcatgctcatcattcaaccaccctccacatctgcatactcaatgaagtgtttga 255

QY 404 aacaaagacatgctttatcatcgtlcatcgtlaacttgcataaaatggaagaatgtttgata 463

Db	256	gaacagcagcagaagatcgtgatacgicagaygagltatgcacagccgggagcgacattatgacta	315
OY	464	tttgacttccaaacgagcaccgtgagtgaagaacagagcgccggaaagaattctcggcaaatcct	523
Db	316	catcagcgagcgagcagacagatccagtgagcggagaagctaaagcattcttccggagatcgt	375
OY	524	gtcggccggtgagtactgttcaacgacatcaatcgtctccacccggagactcaagaacggagaa	583
Db	376	ctctgcgcgtgacatattgcccatacgaacaaagattgtccacccgaatctccaagcttgagaa	435
OY	584	ccctccgtctgataygcaacaatgagacatacgaagcttgcagaaattctgaaatttggaaattcca	643
Db	436	catcctcttgataatgcacatgagaaatcaacgaattgctgacttcggctctccaaactcta	495
OY	644	caagatcagagagacctctgtccacgtygtgtgtagcccccgtatagccgccccggagaat	703
Db	496	ccataaagcgaagtctctgcagaaatctcttgtagagccctctcaatgctctcgcgcgaagat	555
OY	704	ctttgagggagaaagatgatgaagccccccagcttgagacatctggagccttggcgctggtgact	763
Db	556	gttcaatvggaaagccctcaacaagccccagaggtgtagaagctgtgtcccttggtgttccct	615
OY	764	gtacgcttccctgttctcgtgttctctcccttcogaltvggacgtaaacctgcggaagctgagaca	823
Db	616	ctaacactctgtgtgacagacacatgcctcttgtagggcagatgacataagatactcaatgtaa	675
OY	824	gcggtgtgcttgtagagggccgcttcgcgcgacatccgccttctcatgtctcaaaagactgtaagaacct	883
Db	676	acaaatcagcaacggtgacctacgcggagagccacaaacctctgatatgctctgtg---gcct	722
OY	884	gattccacgcagatcgtctgtgtgtgtagaaccccgccaagctgacatacgaatccagatccggca	943
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Search completed: March 22, 2002, 13:26:03
Job time: 7106 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 11:27:37 ; Search time 238.82 Seconds

(without alignments)
9093.061 Million cell updates/sec

Title: US-09-787-559-1

Perfect score: 2533
Sequence: 1 ggcacccaggtgcgcgcgga.....aaaaaaaaaaaaaaaa 2533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2533	100.0	2533	21	AAx82951 Human keratinocyte
2	2522.8	99.6	2632	21	AAx82952 Human keratinocyte
3	2326.6	91.9	2361	22	AA506718 Polynucleotide seq
4	634.2	25.0	640	21	AAC68862 Human protein frag
5	511	20.2	5163	22	AAAF4658 Novel protein kina
6	384.2	15.2	4321	22	AAAF4652 Novel protein kina
7	373.8	14.8	3957	21	AAC77495 Human ORFX ORF3050
8	345.6	13.6	1594	22	AAAF4655 Novel protein kina
9	285.4	11.3	2190	22	AAAF4654 Novel protein kina
10	285.4	11.3	2698	19	AAV03002 Human Twenty-five
11	279.2	11.0	3857	22	AAF85148 DNA encoding a dis

12	279.2	11.0	4790	22	AAF85149 DNA encoding a dis
13	247.6	9.8	1888	21	AAC76944 Human ORFX ORF2499
14	231.6	9.1	2291	22	AAAF4659 Novel protein kina
15	227.2	9.0	3200	22	AAAF7538 Human TGF-beta rec
16	219.6	8.7	2385	22	AA506717 Polynucleotide seq
17	216	8.5	666	22	AAH99147 Murine EST-derived
18	214.4	8.5	2902	22	AAC90433 Murine lymph node
19	211.8	8.4	610	20	AAV87997 EST clone E118.
20	203.2	8.0	2761	16	AAO76197 CDNA of rat liver
21	192.6	7.6	1647	18	AAH85925 Mammalian AMPK alp
22	191.2	7.5	1792	21	AAC44825 Arabidopsis thalia
23	189	7.5	711	22	AAH99224 Human protein enco
24	188.2	7.4	871	22	AAH05352 Human cDNA clone (
25	188.2	7.4	2720	22	AAH15935 Human cDNA sequenc
26	187.8	7.4	1311	22	AA506713 Polynucleotide seq
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28	180.8	7.1	2543	21	AAAF52774 Soybean putative c
29	178.2	7.0	1929	22	AAAF62011 Tomato LESTN1 (suc
30	177.6	7.0	1356	14	AAO47789 SHP gene. Yeast
31	177	7.0	1783	16	AAO76198 CDNA of human aden
32	171.6	6.8	1948	21	AAAF5268 Corn putative cata
33	171.4	6.8	2107	21	AAAF5269 Wheat putative cata
34	167.2	6.6	2006	21	AAAF52777 Novel protein kina
35	166	6.6	1332	22	AAAF4713 Human kinase (PKIN
36	166	6.6	1381	22	AAO08639 Human kinase (PKIN
37	165.6	6.5	1104	22	AAO08637 Polynucleotide seq
38	165.6	6.5	1125	22	AAAF8368 Human SER3 nucleot
39	165.6	6.5	1140	22	AAAF8367 Soybean putative c
40	165.6	6.5	1125	22	AAAF8368 Human SER3 nucleot
41	165.6	6.5	2123	21	AAAF52772 Arabidopsis thalia
42	163.8	6.4	1485	21	AAC46066 Polynucleotide seq
43	161	6.4	2258	22	AAAF52720 Soybean putative c
44	158.8	6.3	2040	21	AAAF52773 zea mays DNA fragm
45	158.2	6.2	1601	21	AAAF51677

ALIGNMENTS

RESULT 1					
ID	AAx82951	standard; cDNA; 2533 BP.			
XX	AAx82951:				
XX	07-JUL-2000	(first entry)			
DE	Human keratinocyte derived pke#122 encoding cDNA #1.				
XX					
KW	Keratinocyte; regulatory protein; human; pke#122; antiproliferative;				
KW	kinase; signal transduction; desmosome; dermatological condition;				
KW	pemphigus vulgaris; psoriasis vulgaris; epidermis; cosmetic; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200017232-A2.				
XX					
PD	30-MAR-2000.				
XX					
PF	06-SEP-1999;	99NO-DE02865.			
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PR	19-SEP-1998;	98DE-1042863.			
XX					
PA	(KRAM/) KRAMER M				
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PI	Kramer M, Bechtel M, Reinartz J, Schaefer B, Wallich R;				
DR	WPI: 2000-283542/24.				
XX					
DR	P-PDB: AAF90878.				
XX					
PT	New regulatory polypeptide from keratinocytes; useful for diagnosis and				
XX	treatment of dermatological disorders; also in cosmetics				

PS Claim 2; Page 49; 55pp; German.

XX This invention describes a novel human regulatory polypeptide designated
CC pKer122 (I), or its variants from human keratinocytes, which in activated
CC keratinocytes is the same as, or similar to, the most highly expressed
CC protein and has antiproliferative activity. (I) is a kinase involved in
CC signal transduction and is conjectured to be involved in cell-cell or
CC cell-matrix interactions and/or formation of (hemi)desmosomes. Modulation
CC of (I) will affect proliferation and differentiation of keratinocytes.
CC (I) is upregulated in some dermatological conditions, e.g. pemphigus
CC vulgaris and psoriasis vulgaris. (I) is used to raise specific antibodies
CC (Ab) which are used for diagnosis and treatment of dermatological
CC disorders and for cosmetic treatment of the epidermis. Nucleic acid (II)
CC that encodes (I) is used; (I) to produce transgenic mammals (particularly
CC mice and rats); and (II) as source of sense and antisense
CC oligonucleotides for diagnosis and treatment of dermatological disorders
CC and for cosmetic treatment of the epidermis. (II), (I) and polypeptides
CC (Ia) produced by splice variants of (II) are used to identify specific
CC binding agents (potentially useful in medicine and cosmetics) that
CC modulate their function and/or expression, especially inhibitors and
CC activators. Cells and animals transformed with (II) are used to study
CC (I)-induced changes in cell morphology and basic functions. This
CC sequence encodes the human keratinocyte protein pKer122 described in the
CC method of the invention.

XX Sequence 2533 BP; 501 A; 820 C; 762 G; 450 T; 0 other;

Query Match 100.0%; Score 2533; DB 21; Length 2533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 tggcgaaagcgacatctcggtcggtgaagctgcgcgcatcgagtcacacaaacgag 180
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RESULT 2
AAx82952 standard; cDNA; 2632 BP.
ID AAx82952 standard; cDNA; 2632 BP.
AC AAx82952;
XX
XX 07-JUL-2000 (first entry)
XX
XX Human keratinocyte derived pKex122 encoding cDNA #2.
XX
XX keratinocyte: regulatory protein: human: pKex122; antiproliferative;
XX kinase; signal transduction; desmosome; dermatological condition;
XX pemphigus vulgaris; psoriasis vulgaris; epidermis; cosmetic; ss.
XX
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OS Homo sapiens.
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XX WO200017232-A2.
XX
XX 30-MAR-2000.
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XX 06-SEP-1999; 99WO-DE02865.
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XX 19-SEP-1998; 98DE-1042863.
XX
XX (KRAM/) KRAMER M.
XX
XX Kramer M, Bechtel M, Reinartz J, Schaefer B, Wallich R;
XX
XX WPI: 2000-283542/24.
XX
XX P-PSDB: AAM90879.
XX
XX New regulatory polypeptide from keratinocytes, useful for diagnosis and
XX treatment of dermatological disorders, also in cosmetics
XX
XX Claim 2; Page 55; 55pp; German.
XX
XX This invention describes a novel human regulatory polypeptide designated
XX pKex122 (I), or its variants from human keratinocytes, which in activated
XX keratinocytes is the same as, or similar to, the most highly expressed
XX protein and has antiproliferative activity. (I) is a kinase involved in
XX signal transduction and is conjectured to be involved in cell-cell or
XX cell-matrix interactions and/or formation of (hemi)desmosomes. Modulation
XX of (I) will affect proliferation and differentiation of keratinocytes.
XX (I) is upregulated in some dermatological conditions, e.g. pemphigus
XX vulgaris and psoriasis vulgaris. (I) is used to raise specific antibodies
XX (Ab) which are used for diagnosis and treatment of dermatological
XX disorders and for cosmetic treatment of the epidermis. Nucleic acid (II)
XX that encodes (I) is used: (1) to produce transgenic mammals (particularly
XX mice and rats); and (11) as source of sense and antisense
XX oligonucleotides for diagnosis and treatment of dermatological disorders
XX and for cosmetic treatment of the epidermis. (II), (I) and polypeptides
XX (Ia) produced by splice variants of (II) are used to identify specific
XX binding agents (potentially useful in medicine and cosmetics) that
XX modulate their function and/or expression, especially inhibitors and
XX activators. Cells and animals transformed with (II) are used to study
XX CC (I)-induced changes in cell morphology and basic functions. This
XX CC sequence encodes the human keratinocyte protein pKex122 described in the
XX CC method of the invention.
XX
XX Sequence 2632 BP: 513 A; 852 C; 809 G; 458 T; 0 other:
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XX
XX Query Match 99.6%; Score 2522.8; DB 21; Length 2632;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 827 ggtgtctgagagggcgctctccgacatccctctctcatgtctcaagaactgtgaagcctgat 886
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Db 887 ccgcgcgacatgctgtgtgtgaaccccgacagcgacatacgaacccgaatcccgagaga 946
QY 848 ccggtgtgagctgagcgtctgaacccctgtgcccggagaccccgccctctccgacaga 907
Db 947 ccggtgtgagctgagcgtctgaacccctgtgcccggagaccccgccctctccgacaga 1006
QY 908 ccggtgtgacactccaaactctggcgacatgaatgaagcgtcggtgtatcatgacaccc 967
Db 1007 ccggtgtgacactccaaactctggcgacatgaatgaagcgtcggtgtatcatgacaccc 1066
QY 968 ggcgctgtgagccgagcagagagacggtgtgagatcaactgtgcaaaacagacataacacactgtgc 1027
Db 1067 ggcgctgtgagccgagcagagagacggtgtgagatcaactgtgcaaaacagacataacacactgtgc 1126
QY 1028 tgcacatttatcctcctcctctgtgacggtcgaagagatctcggaatgcccaatgtgcgcg 1087
Db 1127 tgcacatttatcctcctcctctgtgacggtcgaagagatctcggaatgcccaatgtgcgcg 1186
QY 1088 ccccgagcctgtgcagagcagccgagcctgcgagcctgcgagacccaagtggtcttggaagtgc 1147
Db 1187 ccccgagcctgtgcagagcagccgagcctgcgagcctgcgagacccaagtggtcttggaagtgc 1246
QY 1148 tcagagagagtgctttcacacgacaccccttcgcgaactgtgctgtgtgcgagccagccgagagac 1207
Db 1247 tcagagagagtgctttcacacgacaccccttcgcgaactgtgctgtgtgtgcgagccagccgagagac 1306
QY 1208 ctgtgtgtgagctccgtctcctccagcagagatgtgactgtgagctccagagctctgtcagtg 1267
Db 1307 ctgtgtgtgagctccgtctcctccagcagagatgtgactgtgagctccagagctctgtcagtg 1366
QY 1268 ggcctgtgtcttcctccggtgagatgtgcagctgtgcagcgagatgtgtccggcccccgcgctgtgc 1327
Db 1367 ggcctgtgtcttcctccggtgagatgtgcagctgtgcagcgagatgtgtccggcccccgcgctgtgc 1426
QY 1328 cccaagcagcctgtgagacagccaatcagatgagagagccagggccagggccctagaga 1387
Db 1427 cccaagcagcctgtgagacagccaatcagatgagagagccagggccagggccctagaga 1486
QY 1388 ggaagagcagagacagcagagatccctgtccagcagacagggccggagacacacccctgtgc 1447
|||||

Db 1487 ggaagagcagagacagcagagatccctgtccacagcagcgccgagacacacccctgtgc 1546
QY 1448 cgaaggtctccacccgctctctccacatccacccgacatgtatgtgtgtcccccctccac 1507
Db 1547 cgaaggtctccacccgctctctccacatccacccgacatgtatgtgtgtgtcccccctccac 1606
QY 1508 cagcgcaagtctgtcagagaggaacagactctgaaagtgtgtcgaactctctctgtcagagaa 1567
Db 1607 cagcgcaagtctgtcagagaggaacagactctgaaagtgtgtcgaactctctctgtcagagaa 1666
QY 1568 aagcccgcgaggtctcagctgagcaccccgacacactaagggctgtcgtgcgtctcc 1627
Db 1667 aagcccgcgaggtctcagctgagcaccccgacacactaagggctgtcgtgcgtctcc 1726
QY 1628 ggtcaagctgtgctcgtccgacccctcctgggtgtgcgaatctccgacaccccaagtgtctcagagctca 1687
Db 1727 ggtcaagctgtgctcgtccgacccctcctgggtgtgcgaatctccgacaccccaagtgtctcagagctca 1786
QY 1688 gggggctgtgagagagctgtctcgtccctgtcaagcttccagagagggagcgcgctgc 1747
Db 1787 gggggctgtgagagagctgtctcgtccctgtcaagcttccagagagggagcgcgctgc 1846
QY 1748 ggaacactcaactgaactcaagggctgaaggtcttcgcgagagagctgtgagagacacagcg 1807
Db 1847 ggaacactcaactgaactcaagggctgaaggtcttcgcgagagagctgtgagagacacagcg 1906
QY 1808 gaccaaaaggtgttctgtgagactgaaacaaatcaaggggtgtgctgcagagtgtgtcagagt 1867
Db 1907 gaccaaaaggtgttctgtgagactgaaacaaatcaaggggtgtgctgcagagtgtgtcagagt 1966
QY 1868 ccctgtcagccggggccagcagggcggtgcctgaagcccttccacgcctctgacagagacc 1927
Db 1967 ccctgtcagccggggccagcagggcggtgcctgaagcccttccacgcctctgacagagacc 2026
QY 1928 aggcctgtcagcgcggtgcagagcccgacggagagggctgtgcagagaggtgtgt 1987
Db 2027 aggcctgtcagcgcggtgcagagcccgacggagagggctgtgcagagaggtgtgt 2086
QY 1988 aagagcagcagaggtgtctcagcttcaagcaacacccggcgactgtcacccgggtgtccca 2047
Db 2087 aagagcagcagaggtgtctcagcttcaagcaacacccggcgactgtcacccgggtgtccca 2146
QY 2048 ggcgcgccacgcccgcctgcctgcctgtgtatgtgcgccctgtgtatgtgcccctgtggtgc 2107
Db 2147 ggcgcgccacgcccgcctgcctgcctgtgtgtatgtgcgccctgtgtatgtgcccctgtggtgc 2206
QY 2108 cccggtcccccagcaacccctccacagctgcgggtcccgctgtctgcgcgcccacactgtga 2167
Db 2207 cccggtcccccagcaacccctccacagctgcgggtcccgctgtctgcgcgcccacactgtga 2266
QY 2168 gaccggtgcgtctcccccgtgtgcctcagcgtgcagactccctgtgacacacacactgtacatgtg 2227
Db 2267 gaccggtgcgtctcccccgtgtgcctcagcgtgcagactccctgtgacacacacactgtacatgtg 2326
QY 2228 cagcgccccacacgcccctcccgctgtgtcccccacacagcctgtgacggtcgtgcccag 2287
Db 2327 cagcgccccacacgcccctcccgctgtgtcccccacacagcctgtgacggtcgtgcccag 2386
QY 2288 ttgtgaagccctgtggtgtgcgtgtcagggagactgtgagaatgagacactgtactgtcctgtc 2347
Db 2387 ttgtgaagccctgtggtgtgcgtgtcagggagactgtgagaatgagacactgtactgtcctgtc 2446
QY 2348 cctaagcagcttctgtcctgtgtcagtgagggcagccctgtacatcctgtgcagagacactgtac 2407
Db 2447 cctaagcagcttctgtcctgtgtcagtgagggcagccctgtacatcctgtgcagagacactgtac 2506
QY 2408 tcttaacgcaataacttcaagagaggtgaagacatctgtgcttcaagccaagaacttct 2467
Db 2507 tcttaacgcaataacttcaagagaggtgaagacatctgtgcttcaagccaagaacttct 2566
QY 2468 aagaagcgaataaagcaatacgtgttagtgttctgtgcgaataaataaataaataaataa 2527
Db 2567 aagaagcgaataaagcaatacgtgttagtgttctgtgcgaataaataaataaataaataaataa 2626
|||||


```
QY 1155 ggtcttccacgaccccttccgacctgctgtgtgtcccgacgacgacctgtgtg 1214
    |||
Db 1141 ggtcttccacgaccccttccgacctgctgtgtgtcccgacgacgacctgtgtg 1200
QY 1215 caatcgctctccacgacgacgacgacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1274
    |||
Db 1201 caatcgctctccacgacgacgacgacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 1275 ttcttcctcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1334
    |||
Db 1261 ttcttcctcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
QY 1335 agctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1394
    |||
Db 1321 agctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
QY 1395 caagacacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 1454
    |||
Db 1381 caagacacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 1440
QY 1455 tccacccgctctccacacacacacacacacacacacacacacacacacacacac 1514
    |||
Db 1441 tccacccgctctccacacacacacacacacacacacacacacacacacacacacac 1500
QY 1515 agtctctgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 1574
    |||
Db 1501 agtctctgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 1560
QY 1575 gcgaggtctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1634
    |||
Db 1561 gcgaggtctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1620
QY 1635 ctgggacctgacctctctctctctctctctctctctctctctctctctctctctct 1694
    |||
Db 1621 ctgggacctgacctctctctctctctctctctctctctctctctctctctctctct 1680
QY 1695 ttggaggaagactgtctctctctctctctctctctctctctctctctctctctctct 1754
    |||
Db 1681 ttggaggaagactgtctctctctctctctctctctctctctctctctctctctctct 1740
QY 1755 tcaactgaactcaagagctgtgaagccttctctctctctctctctctctctctctct 1814
    |||
Db 1741 tcaactgaactcaagagctgtgaagccttctctctctctctctctctctctctctct 1800
QY 1815 ggggttctgggactgtgaacaaatcaagagctgtgctgctgctgctgctgctgctgct 1874
    |||
Db 1801 ggggttctgggactgtgaacaaatcaagagctgtgctgctgctgctgctgctgctgct 1860
QY 1875 agccgagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1934
    |||
Db 1861 agccgagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1920
QY 1935 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 1994
    |||
Db 1921 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 1980
QY 1995 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 2054
    |||
Db 1981 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 2040
QY 2055 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 2114
    |||
Db 2041 cagcgagcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 2100
QY 2115 cccagacacccctcctcaagctcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2174
    |||
Db 2101 cccagacacccctcctcaagctcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2160
QY 2175 ggcgcgcccgctgctcagcgacgacgacgacgacgacgacgacgacgacgacgacgacg 2234
    |||
Db 2161 ggcgcgcccgctgctcagcgacgacgacgacgacgacgacgacgacgacgacgacgacg 2220
QY 2235 cccacgcgcctcctcccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2294
    |||
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```
Db 2221 cccacgcgcctcctcccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
QY 2295 cccctgtggtctgtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2354
    |||
Db 2281 cccctgtggtctgtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2340
QY 2355 acgtttgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2375
    |||
Db 2341 acgtttgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2361

RESULT 4
AAC68862
ID AAC68862 standard; cDNA: 640 BP.
XX
AC AAC68862;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human protein fragment PNT065 coding sequence SEQ ID NO: 3.
XX
KM protein-protein interaction; physiological disorder; NIDDM;
KM neurodegenerative disorder; drug screening; predisposition;
KM non-insulin dependent diabetes mellitus; ss.
XX
OS Homo sapiens.
XX
PN WO200065340-A1.
XX
PD 02-NOV-2000.
XX
PE 21-APR-2000; 2000WO-US10651.
XX
PF 22-APR-1999; 98US-0130389.
PR 24-JUN-1999; 98US-0140693.
PR 30-SEP-1999; 98US-0156947.
PR 02-NOV-1999; 99US-0163073.
PR 02-DEC-1999; 99US-0168376.
PR 02-DEC-1999; 99US-0168378.
XX
PA (MYRIAD) MYRIAD GENETICS INC.
XX
PI Heichman K, Bartel PL;
XX
XX WPI: 2000-687376/67.
XX DR P-PSDB: AAB36283.
XX
PT Novel protein complexes involved in mammalian physiological pathways,
PT for diagnosing predisposition to, or existence of diabetes or
PT Alzheimer's disease, and in drug screening for identifying modulators
PT of complexes
XX
PS Claim 42; Page 47; 87pp; English.
XX
CC The present invention relates to novel protein-protein interactions which
CC are involved in mammalian physiological diseases and disorders. These
CC include non-insulin dependent diabetes mellitus (NIDDM) and
CC neurodegenerative diseases such as Alzheimer's disease. The protein
CC complexes described can be used in the diagnosis of these diseases and a
CC predisposition to them, in drug screening and in the identification of
CC other proteins involved in the same pathway.
XX
SQ Sequence 640 BP; 104 A; 228 C; 202 G; 106 T; 0 other;
```

Query Match 25.0%; Score 634.2; DB 21; Length 640;
Best Local Similarity 99.5%; Pred. No. 46-115;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 846 caccggtgatggagctagccctgtcgcggagaccgacctgcccgtcttcgcga 905
Db 1 cgcggtgatggagctagccctgtcgcggagaccgacctgcccgtcttcgcga 60

Qy	906	caagctacacactccaacactctggtgagctactagatagacgaggtgcgtggtatcatatgcaaac	965
Db	61	cacagctacacactccaacactctggtgagctactagatagacgaggtgcgtggtatcatatgcaaac	120
Qy	966	ctggagcgtgagcccgacagagagcgtgtgagatcactgtgcaaaacagacataaacactctt	1025
Db	121	ctggagcgtgagcccgacagagagcgtgtgagatcactgtgcaaaacagacataaacactctt	180
Qy	1026	gctgcacatttatatcaactcctctctgtgagcgtgtcctcaagagatctggaatgcccagtgcc	1085
Db	181	gctgcacatttatatcaactcctctctgtgagcgtgtcctcaagagatctggaatgcccagtgcc	240
Qy	1086	cgccccggtgctctgcacagcgacgcgcgtctctgagatctcgacatcagttggtttgaggtg	1145
Db	241	cgccccggtgctctgcacagcgacgcgcgtctctgagatctcgacatcagttggtttgaggtg	300
Qy	1146	cctcagagaaagttctttccacacgacacctttccgagactcgtcctgtgtgtcccgacacgcag	1205
Db	301	cctcagagaaagttctttccacacgacacctttccgagactcgtcctgtgtgtcccgacacgcag	360
Qy	1206	acctgtgtacgtctccgtctccacagccgagatgagatctgagatctccacagagctctgtcag	1265
Db	361	acctgtgtacgtctccgtctccacagccgagatgagatctgagatctccacagagctctgtcag	420
Qy	1266	tgtgcctctgtctctcccggtgtgatatgcagactgtcagcggagatgtgtccgccccggtcgtg	1325
Db	421	tgtgcctctgtctctcccggtgtgatatgcagactgtcagcggagatgtgtccgccccggtcgtg	480
Qy	1326	tcgccaaagcagctctgtctgagacacagccatcatgtagagagacacagcagagggcgagctta	1385
Db	481	tcgccaaagcagctctgtctgagacacagccatcatgtagagagacacagcagagggcgagctta	540
Qy	1386	gagagagagcagagacagcagagagtlccctgtccacagcagcagcggcgcgagacacactg	1445
Db	541	gagagagagcagagacagcagagagtlccctgtccacagcagcagcggcgcgagacacactg	600
Qy	1446	gcgcgaggtctccacccgctctcccaactacacgcgcga	1484
Db	601	gcgcgaggtctccacccgctctcccaactacacgcgcga	639
RESULT 5			
AAFA4658			
ID	AAFA4658 standard; cDNA; 5163 BP.		
XX	AAFA4658;		
XX	27-MAR-2001 (first entry)		
XX	Novel protein kinase cDNA, SEQ ID NO: 38.		
DE	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;		
KW	immunosuppressive; cardiant; renal; antiinflammatory; antisthmatic;		
KW	dermatological; antidiabetic; antifertility; gene therapy; vaccine;		
KW	immune disorder; cardiovascular disease; neurodegenerative disease;		
KW	cancer; autoimmune disorder; stroke; inflammatory bowel disease;		
KW	inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	MO200073469-A2.		
PN	07-DEC-2000.		
PD	26-MAY-2000; 2000MO-US14842.		
XX	28-MAY-1999; 99US-0136503.		
XX	(SUGEN-) SUGEN INC.		
PA	Plowman GD, Martinez R, Whyte D, Sudersanam S;		
XX			

DR	WP1: 2001-032161/04.
P	P-PSDB; AAB5631.
xx	Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT	treating immune-related diseases and disorders, cardiovascular disease,
PR	neurodegenerative diseases and/or cancers -
xx	
xx	Example 1; Fig 2; 310pp; English.
CC	The present sequence encodes a novel protein kinase. The nucleic acids
CC	and the protein kinases they encode may be used in the treatment and
CC	diagnosis of diseases associated with inappropriate kinase expression
CC	such as immune-related diseases and disorders, cardiovascular disease,
CC	neurodegenerative diseases and/or cancers. The nucleic acids and
CC	complementary sequences may also be used as DNA probes in diagnostic
CC	assays. The kinase polypeptides may be used as antigens in the production
CC	of antibodies of kinase expression and activity. Anti-kinase antibodies
CC	and kinase antagonists may also be used to down regulate kinase
CC	expression and activity. Diseases related to kinase expression and
CC	activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC	disorders, complications of organ transplantation, myocardial infarction,
CC	immune disorders, cardiomyopathies, strokes, renal failure,
CC	oxidative-stress related disorders, chronic inflammatory bowel disease,
CC	chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC	osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC	reproductive disorders.
SO	Sequence 5163 BP; 1336 A; 1352 C; 1266 G; 1207 T; 2 other;
Query Match	20.2%; Score 511; DB 22; Length 5163;
Best Local Similarity	69.5%; Pred. No. 7.5e-91;
Matches 707; Conservative 1; Mismatches 306; Indels 3; Gaps 1;	
OY	55 ccgcggcgccagcgtcaaggccacgaagaagcccccttcggttggttttaagcacatcgagc 114
Dd	165 cggatggtgccgggggaccttgcgcgcggcgccgcctgcgggtgggtgtcttagcacatcgaa 224
OY	115 ggaacccttgggcaaaagacaacttcgcggttgbtgaagctggcgcgcatcgagtcaccacaaa 174
Dd	225 gcacgcttggcgcaagcgcaacttcgctgtgtgtgtgaagcttggggcgcgacatgaccacaga 284
OY	175 cgacgttgtccaataaabaatttgataaacaacgatltagatccaagtcaaatttggsgaaaa 234
Dd	285 cggaggttgcgaataaanaaatcatcgataagcttcacgctgagtgcagtgaaccttggagaaa 344
OY	235 tctatcgtgagagttcagctcgtatgaagcttctgaaccatccacaactcataaagctttacc 294
Dd	345 tctaccggagaaatlaacaaatlgaaaatlytbltagaccacccctccataatcaaacctttacc 404
OY	295 aggttatgtgaacaagaagacatgcttttaactgcgtactctaatttcttaaataatggagaaa 354
Dd	405 aggtatagtagagaccaaaagtatgtgtgtactctgtgtacagaatatatgcacaaaatvgagaaa 464
OY	355 tgatttatatttgacttccaaacggcgacacttgatgagagacgagcgcggaagaagttct 414
Dd	465 tttttgactatcttgctaatacatgaccggttaatlgaagtcgtgaagccagcgcaaatctct 524
OY	415 ggcaaatccctgcgcgcgtgtgagtactgttcaagaccatcatcacttgttccaccggagactca 474
Dd	525 ggcaaatccctgcgcgtgttgaattatgttcatgagtcggaagatttgtaccacgtgacacca 584
OY	475 agacggagaaacctctgcctgcgtatggaacacatgagacataaagcttgacagatttgatgtg 534
Dd	585 aagctgaaatccctctgcctgtgataacacatgaaatataatcaaatlagcagatttcggttttg 644
OY	535 ggaattcttacacagtcagagagacctctgttccacgttggcttgggtggagcccccgttatgcg 594
Dd	645 gaattctttaaaagtggtgaacgtcgtgcgaacatgtgtgtggcaagcccccttatgtcag 704
OY	595 ccccggaagctcttbgaggggaaagagatgaagcccccacgctgtgacatctggagctctgg 654
Dd	705 ccccggaagctcttbtgaaggcagcagatataagagacacacagctgtgacatcttggaaatagg 764

CC diagnosis of diseases associated with inappropriate kinase expression

D0 834 CAGUAAACGCGCCCAACGCCTGGTGTTCATTTCTCCTTG

Qy	829	tcgccagatctcgccagcagcaccggtgtgatctcgagcttgagccctctgtctcgaggaccgcct	888
Db	894	tgagcagatctcgcaagcacaagtgatgtgaagcttagggagcgcgcgaccccaacttgcaca	953
Oy	889	g-----ccgcgccttctcgccagacagcgtctaacctcccaactcggggtgagtaagtagc	942
Db	954	ggttaatagctcggaatcgcaacaactaaagaaagaaagacaggtgagacccctgaaatgag	1013
Oy	943	agcgctgtggtatcatcagacacccctgtggcgtgtgacccgagcagagacggttgagtcactgc	1002
Db	1014	atgtccctctgtggccatcgagagacatggtgactgagcaaaagacagacactgcagtcattaa	1073
Oy	1003	aaacagcagctataaccacttctgtcgtccatttattctcctcctctctgtagcggctcaag	1061
Db	1074	gatcagatcgtcctatgatacctacatagtgcaatctacagcctctgtgtgtgacataag	1132
RESULT 7			
AAC77495			
ID	AAC77495 standard; cDNA; 3957 BP.		
AC	AAC77495;		
XX	08-FEB-2001 (first entry)		
DT	Human ORF3050 polynucleotide sequence SEQ ID NO:6099.		
DE	Human ORF3050 polynucleotide sequence SEQ ID NO:6099.		
KW	Human; open reading frame; ORFX; detection: cytostatic; hepatotropic;		
KW	vulnery; antipsoriatic; antiparkinsonian; neutropic; neuroprotective;		
KW	anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;		
KW	immunosuppressant; thrombolytic; coagulant; vasotropic; antidiabetic;		
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;		
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;		
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;		
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;		
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KW	cholesterol ester storage; systemic lupus erythematosus; infection;		
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KW	bone damage; catilage damage; antiinflammatory disease; coagulation;		
OS	thrombosis; contraceptive; ss.		
XX	Homo sapiens.		
XX	Wo2000058473-A2.		
PN	05-OCT-2000.		
PD	31-MAR-2000; 2000MO-US08621.		
PF	31-MAR-1999; 99US-0127607.		
PR	02-APR-1999; 99US-0127636.		
PR	05-APR-1999; 99US-0127728.		
PR	30-MAR-2000; 2000US-0540763.		
XX	(CURA-) CURAGEN CORP.		
XX	Shimkets RA, Leach M;		
PI	WPI; 2000-602362/57.		
DR	P-PSDB; AAB43286.		
XX	Novel nucleic acids and peptides derived from open reading frame X,		
PT	useful for treating e.g. cancers, proliferative disorders,		
PT	neurodegenerative disorders and cardiovascular disease -		
XX	Claim 5; Page 5283-5285; 5507pp; English.		
PS	AAC77446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,		
CC	which represent the human ORF open reading frames 1 to 3161. The ORF		
CC	sequences have activities such as: cytostatic; hepatotropic; vulnery;		
CC	antipsoriatic; antiparkinsonian; neutropic; neuroprotective;		

CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotonic;
CC antidabetic; hypotensive; dermatolytic; immunosuppressive;
CC antinflammatory; antibacterial; antiviral; antifungal; antihemetic;
CC antihypoid; and antanaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORF α -associated disorder. The
CC nucleic acids can be used to express ORF α proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC noncural haemoglobinuria, antinflammatory disease; to enhance
CC coagulation; to inhibit Thrombosis; and as a contraceptive.
XX Sequence 3957 BP; 983 A; 1164 C; 979 G; 831 T; 0 other;

Query Match	14.8%	Score 373.8;	DB 21;	Length 3957;
Best Local Similarity	66.4%;	Pred. No. 4.7e-64;		
Matches 537; Conservative	0;	Mismatches 272;	Indels 0;	Gaps 0;

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QY	109	tcgag	cggagcc	cttg	gcaag	gcaacttc	cg	ggtgtg	tgaag	cgtcg	cgcatcg	tca	168	
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2522.8	95.9	2533	6 AX024729	AX024729 Sequence
3	2326.6	88.4	2361	6 AX166527	AX166527 Sequence
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6	1575.2	59.8	4498	10 MMU01494	MMU01494 Mus muscu
7	1060.2	40.3	5115	5 AF219232	AF219232 Gallus ga
8	509.8	19.4	4868	6 AX086548	AX086548 Sequence
9	509.8	19.4	4868	6 HSM081732	HSM081732 Sequence
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11	508.2	19.3	2213	9 AK000396	AK000396 Homo sapi
12	506.4	19.2	148463	2 AC012140	AC012140 Homo sapi
13	506.4	19.2	158063	9 AP001046	AP001046 Homo sapi
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16	466	17.7	4626	9 AB018324	AB018324 Homo sapi
17	389.4	14.8	4460	9 AB023216	AB023216 Homo sapi
18	382.6	14.5	4321	6 AX056387	AX056387 Sequence
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ALIGNMENTS

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DEFINITION Sequence 4 from Patent WO0017232.
ACCESSION AX024732
VERSION AX024732.1 GI:10184809

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 2632)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.
TITLE Regulatory protein from human keratinocytes
JOURNAL Patent: WO 0017232-A 4 30-MAR-2000;
REINARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ;
SCHAEFER BIRGIT (DE) ; WALICH REINHARD (DE)

FEATURES
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VERSION	AX024729.1	GI:10184808	
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REFERENCE		1 (bases 1 to 2533)	
AUTHORS		Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.	
TITLE		Regulatory protein from human keratinocytes	
JOURNAL		Patent: WO 0017232-A 1 30-MAR-2000;	
		REINARTZ, JEANETTE (DE) ; BECHTEL, MICHAEL (DE) ; KRAMER, MICHAEL (DE)	
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VERSION AX166527.1 GI:14546872
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REFERENCE 1 (bases 1 to 2361)
AUTHORS Plozman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 18 31-MAY-2001;
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DEFINITION
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ACCESSION
AF106937.1 GI:6492127
VERSION

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DEFINITION	Rattus norvegicus mRNA for salt-inducible protein kinase, complete cds.		
ACCESSION	AB020480		
VERSION	AB020480.1	GI:5672675	
KEYWORDS	SIR: salt-inducible protein kinase.		
SOURCE	Rattus norvegicus (strain:Sprague-Dawley) 6 week old male adrenal gland cDNA to mRNA.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (sites)		
AUTHORS	Wang,Z., Takemori,H., Halder,S.K., Nonaka,Y. and Okamoto,M.		
TITLE	Cloning of a novel kinase (SIR) of the SNF1/AMPK family from high salt diet-treated rat adrenal		
JOURNAL	FBS Lett. 453 (1-2), 135-139 (1999)		
REFERENCE	99330184		
AUTHORS	2 (bases 1 to 2650)		
TITLE	Wang,Z.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (25-NOV-1998) to the DDBJ/EMBL/Genbank databases.		
AUTHORS	Zhi-nong Wang, Osaka University Medical School, Dept. Molecular Physiological Chemistry: 2-2 Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail: wznnong@mr-mbio.med.osaka-u.ac.jp, Tel:81-6-879-3286, Fax:81-6-879-3289)		
COMMENT	Sequence updated (28-Apr-1999).		
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 1 (bases 1 to 5115)
 Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,J.
 The new serine-threonine kinase, q1k, is a target of the q1n
 oncogene
 JOURNAL Biochem. Biophys. Res. Commun. 276 (2), 564-570 (2000)
 MEDLINE 20484194
 PUBMED 11027514
 2 (bases 1 to 5115)
 XIA,Y., ZHANG,Z., KRUSE,U., VOGT,P.K. and LI,J.
 Direct Submission
 Submitted (27-DEC-1999) Molecular and Experimental Medicine, The
 Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla,
 CA 92037, USA
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DB 690 CTGAGTTCCTGCTGCTTTTGTGAGACCAATCTTCAACTGTGAGGCAAGAGTGTGGA 749

QY 836 gggcgcttcgcacatccctctcattcgtctcaagactgtgagagctgtatccgcgcat 895  
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QY 896 gctgtgtgtgaagcccgagagcgatcaacatcgccccagatcccgagcaagctgtgat 955  
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QY 1784 tcaggggggtcttggagagagctgtctgtcctcctgtcaagcttccaggaagcgcgagc 1843


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DEFINITION	HSMB01732 4868 bp mRNA PRI 10-MAR-2001
ACCESSION	Homo sapiens mRNA; CDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds.
VERSION	AL136764
KEYWORDS	AL136764.1 GI:12053044
ORGANISM	human.
REFERENCE	Homo sapiens Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 4868) Wiemann,S., Well,B., Wellenreuther,R., Gassenhuber,J., Glasl,S., Ansojge,W., Boecker,M., Bloecker,H., Battersachs,S., Blum,H., Lauber,J., Duesterhoeft,A., Beyer,A., Koehner,K., Strack,N., Mewes,H.W., Ostenvaelder,B., Obermaler,B., Tampe,J., Heubner,D., Wombolt,R., Korn,B., Klein,M. and Poustka,A. Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs Genome Res. 11 (3), 422-435 (2001)
JOURNAL	2 (bases 1 to 4868) Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission Submitted (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY
REFERENCE	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBR (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
AUTHORS	This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/ . Location/Qualifiers
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Query Match	19.4%	Score 509.8;	DB 9;	Length 4868;
Best Local Similarity	69.5%;	Pred. No. 2.2e+85;		
Matches 707;	Conservative 0;	Mismatches 307;	Indels 3;	Gaps 1;
polya_signal	4777. .4782			
polya_site	4798			
BASE COUNT	1279 a	1259 c	1190 g	1140 t
ORIGIN				
Query Match	19.4% <td>Score 509.8; <td>DB 9; <td>Length 4868; </td></td></td>	Score 509.8; <td>DB 9; <td>Length 4868; </td></td>	DB 9; <td>Length 4868; </td>	Length 4868;
Best Local Similarity	69.5%;	Pred. No. 2.2e+85;		
Matches 707;	Conservative 0;	Mismatches 307;	Indels 3;	Gaps 1;
polya_signal	4777. .4782			
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BASE COUNT	1279 a	1259 c	1190 g	1140 t
ORIGIN				


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ORIGIN

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OY 214 ggaacctgggcaaggaaggaacttcgggtgtgtgaagctggcgcgatcgagtcacaaa 273
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Db 150 GCAAGCTGGGCAAGGCGCACTTCGCTGTGTGAAGCTGGGCGCGCACCGATCCACAGA 209
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 274 cgcaggtgtcaataaataatgataaacaacagatgattcaagaatttggagaataa 333
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 210 CGGAGGTGGCAATTAATATGATATGATCTGAGTGTGATGAGTGTGAGTGTGAGTAA 269
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OY 334 tctatcgtagagtcagagtcagatccttcgaacacatccacatcataaagcttacc 393
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Db 270 TCTACCGAGAGTAAATTAATGAATATGTTAGACACACCTCATATATCAACTTTATC 329
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OY 394 aggttatgaaacaagaagacatcttacatcgctactgaattgtctaaatgagaaa 453
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OY 814 cgcgtgaagacggcggtgctgtagggcgccgtctccacacacacacacacacacacac 873
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OY 874 gtgagagcctgcatccgcgcagatctggtgtagcccgccagcgacatcacacacacac 933
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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OY 934 agatcgagcagacacgggtgtagtcgggctgagccctgttcgcgagacccgcgtcccg 993
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OY 994 cctctcgcagacagctacacacacacacacacacacacacacacacacacacacacac 1053
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OY 1114 ataaccacttgcgtccattatctaccctcccttcggcgagcgaagagatcga 1170
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ORGANISM
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
1 (bases 1 to 148463)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-10M14
Unpublished
2 (bases 1 to 148463)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Feireira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardy, S., Grant, G., Hages, B., Heath, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., MacDonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
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TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced g1:6454007.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L3106
Center Clone name: 10_M_14
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135488 bases at least Q40
Consensus quality: 141694 bases at least Q30
Consensus quality: 144517 bases at least Q20
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Insert size: 146863; sum-of-ctlgts
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctlgts

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

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JOURNAL Submitted (12-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular
Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan
(E-mail: nshimizu@med.keio.ac.jp, Tel: 81-3-3351-2370,
Fax: 81-3-3351-2370)

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Best Local Similarity 99.8%; Pred. No. 5,2e-85;
Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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VERSION AP001751.1 GI:7768753
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REFERENCE
1 (sites)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
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Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstieck,G.,
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Reichelt,J., Kauer,G., Bioecker,H., Ramser,J., Beck,A., Klages,S.,
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Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.

TITLE
JOURNAL
REFERENCE
MEDLINE
AUTHORS

Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstieck,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bioecker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.

Direct Submission
Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The
Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic
Sciences Center, Human Genome Research Group * Institute of
Molecular Biotechnology, Genome Analysis * Keio University School
of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
Analysis * Max-Planck Institute for Molecular Genetics (addresses
see below)
On May 30, 2000 this sequence version replaced gi:7717412.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
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Deutendbergstrasse 11, D-07745 Jena, Germany,
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* URL: http://www.dmb.med.keio.ac.jp/
and
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info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.fz-berlin.mpg.de/
AL163296: Submitted (10-Apr-2000).
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Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 179556)
Waterston, R.H.
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (17-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced g1:7023168.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WTGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0351D02
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Chemistry: Dye-terminator Big Dye; 0% of reads
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Quality coverage: 5.54 in Q20 bases; agarose-fp
Quality coverage: 5.64 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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